

GenCore version 5.1.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 12, 2003, 20:08:49 ; Search time 1995 Seconds
(without alignments)
3603.205 Million cell updates/sec

Title: US-09-705-500A-3
Perfect score: 1268
Sequence: 1 MLQNSAVLLVLVISATHE.....NLRGEDSPSHIKRTSHESA 247

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-O=/cgn2.1/USPTO.spool/US09705500/runat_06062003.113612.7454/app.query.fasta_1.391
-DB=GenEmbl -OPWT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOFC=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSZE=500 -MINLEN=0 -MAXLEN=2000000000
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-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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41: em.htgo.other.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1268	100.0	741	6	E37712	E37712 Osteogenesi
2	1268	100.0	741	6	E39295	E39295 Novel prote
3	1268	100.0	771	6	AR055558	AR055558 Sequence
4	1268	100.0	771	6	AR091578	AR091578 Sequence
5	1268	100.0	840	9	HSU46768	U46768 Human stann
6	1268	100.0	2481	9	BC029044	BC029044 Homo sapi
7	1268	100.0	3901	9	HSU25997	U25997 Homo sapien
8	1234	97.3	1232	10	MMU47815	U47815 Mus musculu
9	1231	97.3	2341	10	BC021425	BC021425 Mus muscu
10	1231	97.1	1004	10	RNU62667	U62667 Rattus norv
11	1228	96.8	4183	10	AF099098	AF099098 Mus muscu
12	1199	94.6	834	4	AF257506	AF257506 Bos tauru
13	861	67.9	585	6	AX156292	AX156292 Sequence
14	682	53.8	2192	5	ANGCSPA	M38967 Anguilla au
15	680.5	53.7	2190	6	A05174	A05174 Synthetic n
16	662.5	52.2	1743	5	AF326317	AF326317 Oncorhync
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18	662.5	52.2	1934	5	S59519	S59519 stannlocalc
19	654	51.6	2807	5	AB060558	AB060558 Osteoglos
20	617	48.7	555	5	S80134	S80134 Oncorhynch
21	515	40.6	177104	10	AC091237	AC091237 Mus muscu
22	510	40.2	4479	9	AF098463	AF098463 Homo sapi
23	508	40.1	420	6	AX156284	AX156284 Sequence
24	480	37.9	18216	9	AF242179	AF242179 Homo sapi
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27	354.5	28.0	1004	10	AF056244	AF056244 Mus muscu
28	354.5	28.0	1649	10	BC012206	BC012206 Mus muscu
29	354.5	28.0	1793	10	AF031035	AF031035 Mus muscu
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ALIGNMENTS

RESULT 1

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421 AACCTGAGCCATCACTAGGCTGCTCCAGCTGCCCAATCACTTCTCCACAGATACTAT 480
161 AsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp 180
481 AACAGACTTGTCCGAGGCTGCTGGAAATGTGATGAAGACACAGTCAGCAACAATCAGAGAC 540
181 SerLeuMetGluIysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
541 AGCCTGATGAGAAAAATTGGCCCTAAACATGGCCAGCCTCTTCCACATCTCTGCAGACAGAC 600
201 HisCysAlaGlnThrHisProArgAlaAAspPheAsnArgArgThrAsnGluProGln 220
601 CACTGTGCCCAACACACCCACAGCTGACTTCAACAGGAGAGCCACCAATGAGCCGAG 660
221 LysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHisIleLys 240
661 AGCTGAAGTCTCTCTCAGAACTCCGAGGTGAGGAGGACTCTCCCTCCACATCATA 720
241 ArgThrSerHisGluSerAla 247
721 CGCACATCCCATGAGAGTGCA 741

RESULT 2
E39295
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
E39295
Novel protein and process for producing the same.
PAT 31-JAN-2002
E39295
Novel protein and process for producing the same.
E39295.1
GI:18628926
JP 2000239299-A/12.
Homo sapiens.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 741)
Goto,M., Tomoyasu,M., Yamaguchi,K., Kinozaki,M., Shima,N.,
Yasuda,N. and Nakagawa,N.
Novel protein and process for producing the same
Patent: JP 2000239299-A 12 05-SEP-2000;
SNOW BRAND MILK PROD CO LTD
OS Homo sapiens (human)
PN JP 2000239299-A/12
PD 05-SEP-2000
PF 15-FEB-1999 JP 1999036225
PR
PI MASAAKI GOTO,MASAOKI TOMOYASU,KYOJI YAMAGUCHI, PI MASAHIKO
KINOZAKI,
PI NORIYUKI SHIMA,NAOTAKA YASUDA,NOBUAKI NAKAGAWA PC
C07K14/47,C12N5/10,C12N15/09,C12P21/02//A61K31/00,A61K31/00, PC
A61K38/00,
PC (C12P21/02,C12R1:91),C12N5/00,C12N15/00,A61K37/02 CC
FH Key Location/Qualifiers
FT source 1..741
FT Location/Qualifiers
/organism="Homo sapiens (human)".
1..741
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/db_xref="taxon:9606"
BASE COUNT 201 a 209 c 183 g 148 t
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Alignment Scores:
Pred. No.: 1 7e-123 Length: 741
Score: 1268.00 Matches: 247
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-705-500A-3 (1-247) x E39295 (1-741)

Qy 1 MetLeuGlnAsnSerAlaValLeuLeuValLeuValLeuSerAlaThrHisGlu 20
Db 1 ATGCTCCAAATCAGCAGTGTCTGGTCTGGTATCAGTGTCTGCAACCATGAG 60

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Qy	21	AlaGluGlnAsnAspSerValSerProArgLysSerArgVallalaGlnAsnSerAla	40
Db	61	GGCGAGCAGAATGACTCTGTGAGCGCCAGGAAATCCCGAGTGGCGGCCAAAACTCAGT	120
Qy	41	GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu	60
Db	121	GAAGTGGTTCTTGCTCAACAGTGCTCTCAGGTGGCTCGGGGGCTTTTGTATCCCTG	180
Qy	61	GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer	80
Db	181	GAAAACTCCACCTGTGACACAGATGGGATGTATGACATCTGTAATCTCTTTGTATACAG	240
Qy	81	AlaAlaLysPheAspThrGlnGlyAsnAlaPheValLysGlnSerLeuLysCysIleAla	100
Db	241	GCTGTAAATTTGACACTCAGGGAAAGCAATTCGTCAAGAGAGAGCTTAAATGTCATCGCC	300
Qy	101	AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet	120
Db	301	ACGGGGTCACCTCCACAGGTCTTCTCGCCATTCGGAGGTGCTCCACTTTCNAAGGATG	360
Qy	121	IleAlaGluValGlnGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg	140
Db	361	ATTGTGAGGTGCAGGAAGAGTGTCTACAGCAAGCTGAATGTGTGACGATCGCCAAAGGG	420
Qy	141	AsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyr	160
Db	421	AAACCTGAAGCCATCACTCAGGTGCTCGAGTGCCTCAATCACTTCTCCACAGATATCAT	480
Qy	161	AsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp	180
Db	481	ACACAGCTTGCCGAAGCCTGCTGGAATGTGATGAACACAGATCAGCACATCAGAGAC	540
Qy	181	SerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp	200
Db	541	AGCCTGATGGAGAAATTTGGGCCTAAACATGCCAGCCTCTTCCACATCTCTGCAGACAGAC	600
Qy	201	HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgThrAsnGluProGln	220
Db	601	CACTGTGCCCAAACACACCCAGAGCTGACTTCAACAGGAGAGCGCACCAATGAGCCGCGAG	660
Qy	221	LysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHisIleLys	240
Db	661	AGCTGAAAGTCTCTCTCAGGAACTCCGAGGTGAGGAGGACTCTCCCTCCCAATCAAA	720
Qy	241	ArgThrSerHisGluSerAla	247
Db	721	CGCACATCCCATGAGAGTGCA	741

RESULT 3	AR055558	771 bp	DNA	linear	PAT 29-SEP-1999
LOCUS	AR055558				
DEFINITION	Sequence 1 from patent US 5837498.				

ACCESSION	AR055558
VERSION	AR055558.1
	GI:5981135

KEYWORDS

SOURCE	ORGANISM	Unknown.
		Unknown.
		Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 771)

AUTHORS	Olsen, H.S. and Adams, M.D.
TITLE	Cornuscles of stannous protein stan-

JOURNAL
Patent: US 5837498-A 1 17-NOV-1998;

FEATURES

Location/Qualifiers

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source
1. .771
/organism="uniprot"
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BASE COUNT	212 a	214 c	192 a	153 b

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84

Alignment scores:
Pred. No.: 1 78e-123 Length:

Score: 1268.00
Matches: 1268.00

Percent Similarity: 100.00%

Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0
US-09-705-500A-3 (1-247) x AR055558 (1-771)			
Qy	1	MetLeuClnAsnSerAlaValLeuValLeuValIleSerAlaSerAlaThrHisGlu	20
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Qy	21	AlaGluClnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla	40
Db	76	GCGGAGCAGAATGACTCTGTGAGCCCCCAGGAAATCCCGAGTGGCGGCCCAAACTCAGCT	135
Qy	41	GluValValArgCysLeuAsnSerAlaLeuClnValGlyCysGlyAlaPheAlaCysLeu	60
Db	136	GAAATGGTTCGTTGCCCTCAACAGTGCCTCATCAGGTCGGCTGCGGGGCTTTTGATGCGCTG	195
Qy	61	GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer	80
Db	196	GAAACTCCACCTGTGACACAGATGGGATGTATGACATCTGTAAATCTCTCTGTGTACAGC	255
Qy	81	AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAla	100
Db	256	GCTGCTAAATTTGACATCTCAGGGAAGAGCATTCGTCAAAGAGAGCTTAAATATGCATCGCC	315
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Qy	121	IleAlaGluValGlnGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg	140
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Db	436	AACCTTGAAGCCATCACTGAGGTGCTCCAGCTGCCCAATCACTCTCCAAACAGATACTAT	495
Qy	161	AsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp	180
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Qy	181	SerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp	200
Db	556	AGCCTGATGAGAAAAATTGGSCCTTAAATGGCCAGCTCTTCCACATCTCTGAGACAGAC	615
Qy	201	HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgThrAsnGlnProGln	220
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Qy	221	LysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHisIleLys	240
Db	676	AAGCTGAAGATCTCTCTCAGGAACCTCCGAGGTGAGGAGGACTCTCCCTCCACATCAAA	735
Qy	241	ArgThrSerHisGluSerAla	247
Db	736	CGCACATCCCATGAGAGTGCA	756

RESULT 4

AR091578

LOCUS

DEFINITION
ACCESSION

VERSION

KEYWORDS

SOURCE ORGANIZATION

ORGANIZATION

REFERENCES

AUTHORS

FILE
JOURNAL

FEATURES

[illegible]

QY 161 AsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp 180
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 QY 201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgThrAsnGluProGln 220
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BC029044 2481 bp mRNA linear PRI 16-MAY-2002
 LOCUS Homo sapiens, stanniocalcin 1, clone MGC:34539 IMAGE:5191420, mRNA,
 complete cds.
 ACCESSION BC029044
 VERSION BC029044.1 GI:20810067
 KEYWORDS MGC.
 SOURCE Homo sapiens.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 2481)
 Strausberg, R.
 Direct Submission
 Submitted (01-MAY-2002) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LILNL)
 DNA Sequencing by: Baylor College of Medicine Human Genome
 Sequencing Center
 Center code: BCM-HGSC
 Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
 Contact: amg@bcm.tmc.edu
 Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M.,
 Xoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.,
 Richards, S., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LILNL at: <http://image.llnl.gov>
 Series: IRAK Plate: 50 Row: k Column: 5
 This clone was selected for full length sequencing because it
 passed the following selection criteria: matched mRNA gi: 4507264.
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REMARK
 COMMENT

FEATURES
 source

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 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0

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 QY 41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
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 QY 61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
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 QY 81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAla 100
 DB 503 GCTGCTAAATTTGACACTCAGGGGAAAAGCATTCGTCAAGAGAGAGCTTAAATATGCAATGCC 562
 QY 101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
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HSU25997
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DEFINITION Homo sapiens stanniocalcin precursor (STC) mRNA, complete cds.
ACCESSION U25997
VERSION   U25997.1
KEYWORDS  GI:3006202
SOURCE    Homo sapiens.
ORGANISM  Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3901)
AUTHORS   Chang,A.C., Janosi,J., Hulsbeek,M., de Jong,D., Jeffrey,K.J.,
Noble,J.R. and Reddel,R.R.
TITLE     A novel human cDNA highly homologous to the fish hormone
stanniocalcin
JOURNAL   Mol. Cell. Endocrinol. 112 (2), 241-247 (1995)
MEDLINE   96077825
PubMed    7489828
REFERENCE 2 (bases 1 to 3901)
AUTHORS   Chang,A.C., Jeffrey,K.J., Tokutake,Y., Shimamoto,A., Neumann,A.A.,
Dunham,M.A., Cha,J., Sugawara,M., Furuichi,Y. and Reddel,R.R.
TITLE     Human stanniocalcin (STC): genomic structure, chromosomal
localization, and the presence of CAG trinucleotide repeats
JOURNAL   Genomics 47 (3), 393-398 (1998)
MEDLINE   98149987
PubMed    9480753
REFERENCE 3 (bases 1 to 3901)
AUTHORS   Chang,A.C.-M.
TITLE     Direct Submission
JOURNAL   Submitted (02-MAY-1995) Childrens Medical Research Institute, 214
Hawkesbury Road, Westmead, NSW 2145, Australia
REFERENCE 4 (bases 1 to 3901)
AUTHORS   Chang,A.C.-M.
TITLE     Direct Submission
JOURNAL   Submitted (02-APR-1998) Childrens Medical Research Institute, 214
Hawkesbury Road, Westmead, NSW 2145, Australia
REMARK    Sequence update by submitter
COMMENT    On Apr 2, 1998 this sequence version replaced gi:975297.
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 ACCESSION U62667
 VERSION U62667.1 GI:1762530
 KEYWORDS
 SOURCE Rattus norvegicus.
 ORGANISM Rattus norvegicus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 1 (bases 1 to 1004)
 Abe.T., Tanemoto,M., Hall,A.E., Brown,E.M. and Hebert,S.C.
 Molecular cloning and characterization of rat stannioalcin peptid
 Unpublished
 2 (bases 1 to 1004)
 Abe.T., Tanemoto,M., Hall,A.E., Brown,E.M. and Hebert,S.C.
 Direct Submission
 Submitted (01-JUL-1996) Renal Division, Brigham and Women's
 Hospital, 75 Francis Street, Boston, MA 02115, USA
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QY      241  ArgThrSerHisGluSerAla 247
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RESULT 11
AF099098      4183 bp mRNA linear ROD 10-NOV-1998
LOCUS      Mus musculus stanniocalcin precursor, mRNA, complete cds.
DEFINITION      AF099098
ACCESSION      AF099098.1 GI:3851659
VERSION      AF099098.1 GI:3851659
KEYWORDS
SOURCE      Mus musculus.
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Varghese, R., Wong, C.K.C., Doel, H., Wagner, G.F. and DiMattia, G.E.
Comparative Analysis of Mammalian Stanniocalcin Genes
Endocrinology 139, 4717-4725 (1998)
REFERENCE      2 (bases 1 to 4183)
AUTHORS      DiMattia, G.E., Varghese, R. and Wagner, G.F.
TITLE      Direct Submission
JOURNAL      Submitted (16-OCT-1998) Oncology, London Regional Cancer Centre,
790 Commissioners Rd., London, ONT N6C 4L6, Canada
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898..4183

BASE COUNT 1215 a 979 c 798 g 1191 t

3'UTR

ORIGIN

Alignment Scores:

Score: 2.38e-118 Length: 4183

Percent Similarity: 1228.00 Matches: 237

Best Local Similarity: 97.98% Conservatives: 5

Query Match: 95.95% Mismatches: 5

DB: 96.85% Indels: 0

Gaps: 10

US-09-705-500A-3 (1-247) x AF099098 (1-4183)

QY 1 MetLeuGlnAsnSerAlaValLeuValLeuValIleSerAlaSerAlaThrHisGlu 20

Db 154 ATGCTCCAAACTCAGCAGTGATTTCTGGCGTGGTTCATCAGTGCAGCTGCACGCCACGAG 213

QY 21 AlaGluGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40

Db 214 CGGAAACAAAATGATTTCTGTAGCCCCACAGAAAATCCCGGTGGCGCTCAAAATTCAGT 273

QY 41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60

Db 274 GAAGTGGTTCGCTCCCTCAACAGTGCCCTGCAGGTGGCTCGGGGCTTTTGCATGCGCTG 333

QY 61 GluAsnSerThrCysAspThrAspGlyMetTrpAspIleCysLysSerPheLeuTrpSer 80

Db 334 GAAACTCCACATGTGACACAGATGGGATGTACACATTTGTAAATCCTCTTGTACAGT 393

QY 81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAla 100

Db 394 GCTGCTAAATTTGACACTCAGGGAAGAGCAATTTGTCAAAGAGAGCTTAAAGTGCATGCC 453

QY 101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgHet 120

Db 454 AATGGGATCACCTCCAAGGATTCCTTTGCCATTCCGAGGTGTTCCAGAGGATG 513

QY 121 IleAlaGluValGlnGluGlyCysTrpSerLysLeuAsnValCysSerIleAlaLysArg 140

Db 514 ATCCCGAGGTGCAGAGGAGCTGTACAGCAAGCTTAACTTTGCAGCATGCCAAGCGC 573

QY 141 AsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTrpTyr 160

Db 574 AACCGGAAGCCATCACTGAAGTCATACAGCAGCCCAATCACTTCTCCACAGATACTAC 633

QY 161 AsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp 180

Db 634 AACAGACTTGTCCGAAGCCTTCTGGAATGTGATGAAGACACGGTCAGCACATCAGAGAC 693

QY 181 SerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200

Db 694 AGCCTGATGAGAAGATCGGGCCCAACATGGCCAGCTCTTCCACATCCTCCACAGACAC 753

QY 201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgThrAsnGluProGln 220

Db 754 CACTGTGCCACAGACACACCCAGAGCTGACTTCAATAGGAGCGGTACAAATGAGCCACAG 813

QY 221 LysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHisIleLys 240

Db 814 AAGCTGAAAGTCTCTCTCAGGAACCTCCGAGGTGAGGGGAGTCTCTCCCTCACATCAAA 873

QY 241 ArgThrSerHisGluSerAla 247

Db 874 CGCACCTCCCAAGAGAGTGGC 894

RESULT 12

AF257506

LOCUS

DEFINITION

ACCESSION

VERSION

AF257506 834 bp mRNA linear MAM 09-MAY-2000

Bos taurus stanniocalcin mRNA, complete cds.

AF257506

AF257506.1 GI:7739750

[illegible]

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QY 159 TTTTAAAGGLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIle 178
Db 246 TACTATAACAGACTTGTTCGGAAGCCCTGCGAATGTGATGAAGACACAGCTCAGCAATC 305

QY 179 ArgAspSerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGln 198
Db 306 AGAGACAGCTGATGGAGAAATGGGCTTAACATGGCCAGGCTCTTCCACATCTCGAG 365

QY 199 ThrAspHisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgThrAsnGlu 218
Db 366 ACAGACCACTGTGCCCAACACACACCCAGCTGACTTCAACAGGAGAGCGCAATGAG 425

QY 219 ProGlnLeuLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHis 238
Db 426 CCGCAGAACTGAAAGTCTCTCTCAGGAACCTCCGAGGTCGAGGAGACTCTCCCTCCAC 485

QY 239 IleLysArgThrSerHisGluSerAla 247
Db 486 ATCAACGCACATCCCATGAGATGCA 512

RESULT 14
ANGCSPA
LOCUS Anguilla australis corpuscles of Stannius protein (CS) mRNA, linear VRT 18-DEC-1997
DEFINITION complete cds.
ACCESSION M36967
VERSION 1.0
KEYWORDS corpuscles of Stannius protein.
SOURCE Anguilla australis.
ORGANISM Anguilla australis.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Anguilliformes;
Anguillidae; Anguilla.
REFERENCE 1 (bases 1 to 2192)
AUTHORS Butkus,A., Roche,P.J., Fernley,R.T., Haralambidis,J.,
Penschow,J.D., Ryan,G.B., Trahair,J.F., Tregear,G.W. and
Coghlan,J.P.
Purification and cloning of a corpuscles of Stannius protein from
Anguilla australis
Mol. Cell. Endocrinol. 54 (2-3), 123-133 (1987)
88083961
PUBMED 3319739
REFERENCE 2 (bases 1 to 2192)
AUTHORS Roche,P.J.
Direct Submission
Submitted (05-SEP-1990) Medical Lab Science, RMIT, Melbourne 3001,
Australia
REFERENCE 3 (bases 1 to 2192)
AUTHORS Roche,P.J.
Direct Submission
Submitted (17-DEC-1997) Medical Lab Science, RMIT, Melbourne 3001,
Australia
REMARK Sequence update by submitter
COMMENT On Dec 17, 1997 this sequence version replaced gi:210954.
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A05174

2190 bp

DNA

linear

PAT 30-APR-1993

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BASE COUNT 590 a 515 c 483 g 604 t
ORIGIN

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Alignment Scores:
Pred. No.: 1,45e-61 Length: 2192
Score: 682.00 Matches: 138
Percent Similarity: 72.83% Conservative: 47
Best Local Similarity: 54.33% Mismatches: 57
Query Match: 53.79% Indels: 12
DB: 5 Gaps: 6

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US-09-705-500A-3 (1-247) x ANGCSPA (1-2192)

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QY 1 MetLeuGlnAsnSerAlaValLeuLeuValLeuValIleSerAlaSerAlaThrHisGlu 20
Db 122 ATGCTGCGAATGAGTGGGCTAATCCTCAGCTTGTGCTG---GTAACCTGCTGCCTACGAG 178

QY 21 AlaGluGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
Db 179 CAGGATGAGCGGAGCCCTTATCTCCAAGGACAGCGGCTTCTCCGCCAGCAGCCATCT 238

QY 41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
Db 239 GATGTTGCACGCTGTCTGAACGGGGCCCTGCAGGTGGCTGCAGTGCATTTGCCGTGCTT 298

QY 61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
Db 299 GACAACTCCAGCTGCACACACCGGCAATGCATGAATCTCGAGGTCTCTTCTCCACGCT 358

QY 81 AlaAlaLysPheAspThrGlnGlyValAlaPheValLysGluSerLeuLysCysIleAla 100
Db 359 GCTGCAAAATTGACACACAGGGCAAGACTTTTGAAGGAGAGGCTGAAGTGCATAGCC 418

QY 101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
Db 419 AATGGCATCACCTCAAAGTGTCTTACCATCCGCGCTGCTCATCTCTCCAGAAGATG 478

QY 121 IleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
Db 479 ATCTCAGAGGTTTCAGGAGGAGTGTCTATAGCAAACTAGACCTCTGCTCTGTGTGCCAGAGC 538

QY 141 AsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
Db 539 AACCCAGAGGCCCATGGGGGAGGTGGCCAGGTGCCCGCCAGTTCGCCAGCTTCCCAACAGGTACTAC 598

QY 161 AsnArgLeuValArgSerLeuGluCysAspGluAspThrValSerThrIleArgAsp 180
Db 599 AGCACCTGCTGCAGAGTCTTCTGACGTGTGATGAGGACACCGTGGAGCAGGTAGGGGCC 658

QY 181 SerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
Db 659 GGGTGTGGTGTCCCGCTGGAGCCAGAGATGGGGTGTCTTCTCCAGCTCTCTCCAGACCAAG 718

QY 201 HisCys-----AlaGlnThrHisPro---ArgAlaAspPheAsnArgArg 214
Db 719 GCCTGCCCCCGAGCGCGCGGTGGCAGCTGGCCAGTGGGCGAGGAGGAGGAGCTGGCGGC 778

QY 215 ArgThrAsnGluProGlnLysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAsp 234
Db 779 TGGCCCCATGGGGCCCCCATGTTTCAAGATC---CAGCCCAACCTGCGCTCCCGGAC--- 832

QY 235 SerProSerHisIle-----LysArgThrSerHisGluSer 246
Db 833 ---CCCACCCACCTTTTGTGTAAGAAACGCTCGACCGACCTCC 871

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RESULT 15

A05174

LOCUS

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 12, 2003, 20:08:29 ; Search time 221 Seconds
(without alignments)
2516.939 Million cell updates/sec

Title: US-09-705-500A-3

Perfect score: 1268

Sequence: 1 MLQNSAVLLVLVISASATHE.....NLRGEDSPSHIKTSHESA 247

Scoring table:

BGAPOP 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1268	100.0	741	21	AAA97594	Human stanniocalcin
2	1268	100.0	741	21	AAA11145	Human stanniocalcin
3	1268	100.0	744	24	ABL40225	Human stanniocalcin
4	1268	100.0	771	16	AAT02438	cDNA encoding stan
5	1268	100.0	771	21	AAZ39520	Human corpuscles o
6	1268	100.0	1283	22	AAF83297	Human stanniocalci
7	1268	100.0	3762	22	AAF83823	DNA encoding lng10
8	1250	98.6	2572	21	AAF16051	Human prostate can
9	861	67.9	585	22	AAH55624	Human breast tumou
10	661.5	52.2	2191	9	AAH80655	Sequence encoding
11	508	40.1	420	22	AAH55616	Human breast tumou
12	370	29.2	219	22	ABA51055	Human breast cell
13	370	29.2	219	22	ABA69045	Human foetal liver
14	370	29.2	219	22	ABA35989	Probe #1455 for g
15	370	29.2	219	22	AAK17358	Human brain expres
16	370	29.2	219	22	AAK43155	Human bone marrow
17	370	29.2	219	22	AAI23927	Probe #13860 for g
18	370	29.2	219	22	AAI49233	Probe #17919 used
19	370	29.2	219	22	AAI09526	Probe #9517 used t
20	370	29.2	219	24	ABS17231	Human genome-deriv
21	354.5	28.0	888	21	AAZ57117	Mouse stanniocalci
22	354.5	28.0	888	22	AAF31040	Murine stanniocalc
23	354	27.9	882	20	AAZ28026	Adipogenesis inhib
24	354	27.9	882	21	AAA09620	Human adipocytogen
25	354	27.9	906	21	AAZ57116	Human stanniocalci
26	354	27.9	906	22	AAF25370	Nucleotide sequenc
27	354	27.9	906	22	AAF31030	Human stanniocalci
28	354	27.9	909	22	AAH25831	Human adipogenesis
29	354	27.9	1942	22	AAH15669	Human cDNA sequenc
30	354	27.9	4298	22	AAH17879	Human cDNA sequenc
31	352	27.8	892	17	AAT18979	Stanniocalcin alph
32	352	27.8	892	21	AAZ39303	Human stanniocalci
33	328	25.9	198	17	AAT28165	Senescence-related
34	265	20.9	697	22	AAH04989	Human cDNA clone (
35	253	20.0	774	22	AAH06665	Human cDNA clone (
36	214	16.9	362	22	ABA45937	Human breast cell
37	214	16.9	362	22	ABA56464	Human foetal liver
38	214	16.9	362	22	ABA36097	Probe #4563 for ge
39	214	16.9	362	22	AAK04623	Human brain expres
40	214	16.9	362	22	AAK30134	Human bone marrow
41	214	16.9	362	22	AAI14733	Probe #4566 for ge
42	214	16.9	362	22	AAI36098	Probe #4784 used t
43	214	16.9	362	22	AAI04536	Probe #4527 used t
44	214	16.9	362	24	ABS04715	Human genome-deriv
45	95	7.5	4420	22	AAC90043	Human resistin gen

ALIGNMENTS

RESULT 1

AAA97594

ID AAA97594 standard; cDNA; 741 BP.

AC AAA97594;

XX

DT 02-FEB-2001 (first entry)

XX

DE Human stanniocalcin cDNA.

XX

KW Human; stanniocalcin; STC; osteogenesis; bone disease; osteoporosis;
KW mineral metabolism regulator; prophylaxis; therapy; ss.

OS Homo sapiens.

XX

PN JP2000229880-A.

XX

PD 22-AUG-2000.

[illegible]

Db 61 GCGAGCAGATGATCTGTGAGCCCGAGGAATCCGAGTGGCGGCCCAAACTCAGCT 120
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 Qy 81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAla 100
 Db 241 GCTGCTAAATTTGACACTCAGGAAAGCAATTCGTCAAAGAGAGCTTAAATGCAATGCC 300
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 Qy 201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgArgThrAsnGluProGln 220
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 Db 661 AAGCTGAAAGTCTCTCTCAGGAACCTCCGAGGTGAGGAGGACTCTCCCTCCCAACATCAA 720
 Qy 241 ArgThrSerHisGluSerAla 247
 Db 721 CGCACATCCCATGAGAGTGCA 741

RESULT 3

ABL40225

ID ABL40225 standard; cDNA; 744 BP.

XX AC ABL40225;

XX AC ABL40225;

DT 23-MAY-2002 (first entry)

DE Human staniocalcin 1 encoding cDNA.

KW Human; staniocalcin 1; osteopathic; osteogenesis failure; osteoporosis;
 KW bone mass reduction; traumatic bone injury; osteomalacia; bone disease;
 KW rheumatic bone disease; cancer associated bone disease; rachitis;
 KW arthralgia deformans; gene; ss.

XX OS Homo sapiens.

XX FH Key

XX CDS Location/Qualifiers

FT 1..744

FT /*tag= a

FT /product= "staniocalcin 1"

XX PN WO200204013-A1.

XX PD 17-JAN-2002.

XX

PF 10-JUL-2001; 2001WO-JP05962.

XX 11-JUL-2000; 2000JP-0209926.

XX (BMLB-) BML INC.

XX Yoshiko Y, Koide Y, Igarashi A, Takano S, Maeda N, Aubin JE;

XX WPI; 2002-164600/21.

XX P-PSDB; ABB06259.

XX Agent used for treating bone diseases e.g. osteoporosis, traumatic bone

XX injury, osteomalacia, rheumatic bone diseases, bone diseases associated

XX with cancer and arthritis deformans containing staniocalcin 1.

XX Claim 2; Fig 1; 24pp; Japanese.

XX The present invention describes an agent containing staniocalcin 1,

XX particularly of human origin. Staniocalcin 1 has osteopathic activity.

XX The agent can be used for treating diseases relating to osteogenesis

XX failure or reduction in bone mass e.g. osteoporosis, traumatic bone

XX injury, osteomalacia, rheumatic bone diseases, bone diseases associated

XX with cancer, bone diseases due to phosphorus or calcium metabolic error,

XX rachitis and arthritis deformans. The agent increases bone mass. The

XX present sequence encodes human staniocalcin 1.

XX SQ Sequence 744 BP; 203 A; 209 C; 183 G; 149 T; 0 other;

XX Alignment Scores:

XX Pred. NO.: 1.24e-139 Length: 744

XX Score: 1268.00 Matches: 247

XX Percent Similarity: 100.00% Conservative: 0

XX Best Local Similarity: 100.00% Mismatches: 0

XX Query Match: 100.00% Indels: 0

XX DB: 24 Gaps: 0

XX US-09-705-500A-3 (1-247) x ABL40225 (1-744)

Qy 1 MetLeuGlnAsnSerAlaValLeuValLeuValLeuValLeuValLeuValLeuValLeu 20

Db 1 ATGCTCAAAACTCAGCAGTCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 60

Qy 21 AlaGluGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40

Db 61 GCGAGCAGATGATGACTCTGTGAGCCCGAGGAATCCGAGTGGCGGCCCAAACTCAGCT 120

Qy 41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60

Db 121 GAAAGTGGTTCGTGCTCAACAGTGTCTACAGTGGCTGGCGGCTTTTGATGATCGCTG 180

Qy 61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80

Db 181 GAAAACTCCACTGTGACACAGATGGATGTATGACATCTGTAATCTCTTTGTACAGC 240

Qy 81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAla 100

Db 241 GCTGCTAAATTTGACACTCAGGAAAGCAATTCGTCAAAGAGAGCTTAAATGCAATGCC 300

Qy 101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120

Db 301 AACGGGGTCACCTCAAGGCTTCTCGCCATTCGGAGGTGCTCCACTTTCCAAAGGATG 360

Qy 121 IleAlaGluValGlnGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140

Db 361 ATTGCTGAGGTGCAGGAAGAGTGTCTACAGCAAGCTGTAATGTGTGAGCATCGCCAAAGCGG 420

Qy 141 AsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160

Db 421 AACCTGGAAGCCATCAGTGAAGTGTCTGAGTGTCCAGCTGCCCAATCACTTCTCCAAAGATAT 480

Qy 161 AsnArgLeuValArgSerLeuGluCysAspGluAspThrValSerThrIleArgAsp 180

Db 481 AACAGACTTGTCCGAGGCTGTGGAATGTGATGAAGACACAGTCAAGCAATCAGAGAC 540

```

QY 181 SerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
DB 541 AGCCTGATGGAGAAATTTGGGCTTAACATGGCCAGCCTCTCCACATCTCTGCAGACAGAC 600
QY 201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgThrAsnGluProGln 220
DB 601 CACTGTGCCAAACACACCCAGAGTGACTTCAACAGAGAGACGCCAATGAGCGCGAG 660
QY 221 LysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHisIleLys 240
DB 661 AAGCTGAAAGTCTCTCCAGGAACCTCCAGGTGAGGAGGACTCTCCCTCCACATCAAA 720
QY 241 ArgThrSerHisGluSerAla 247
DB 721 CGCACATCCCATGAGAGTGCA 741

RESULT 4
ID AAT02438 standard; cDNA; 771 BP.
AC AAT02438;
XX
XX
DT 19-APR-1996 (first entry)
XX
DE cDNA encoding stannioalcin from Corpuscles of Stannius.
XX
KW stannioalcin; Corpuscles of Stannius; hypocalcaemia; hypercalcaemia;
KW electrolyte disorder; osteoporosis; Paget's disease; treatment; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 16..759
FT /tag= a
FT /product= prepro-stannioalcin
FT mat_peptide 115..757
FT /tag= b
FT /product= mature stannioalcin
FT misc_feature 16..114
FT /tag= c
FT /note= "encodes prepro region"
XX
PN W09524411-A1.
XX
XX
PD 14-SEP-1995.
XX
PF 09-MAY-1994; 94WO-US05136.
XX
PR 08-MAR-1994; 94US-0208005.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX
PI Adams MD, Olsen H;
XX
XX WPI: 1995-328227/42.
XX
XX P-PSDB; AAR84522.
XX
XX Human corpuscles of Stannius polypeptide(s) - used to treat
XX hypercalcaemia, hypocalcaemia and other electrolyte disorders
XX
XX Claim 1; Fig 1; 41pp; English.
XX
XX The cDNA encodes a stannioalcin, a Corpuscles of Stannius polypeptide.
XX Stannioalcin functions as a hypocalcaemic agent, and can be used for
XX the treatment of e.g. electrolyte disorders which lead to renal, bone
XX and heart diseases, hypertension, hypercalcaemia and disorders due to
XX elevated bone resorption, e.g. osteoporosis and Paget's disease.
XX
XX Sequence 771 BP; 212 A; 214 C; 192 G; 153 T; 0 other;
SQ

Alignment Scores:
Pred. No.: 1.31e-139 Length: 771

```

```

Score: 1268.00 Matches: 247
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 16 Gaps: 0

US-09-705-500A-3 (1-247) x AAT02438 (1-771)

QY 1 MetLeuGlnAsnSerAlaValLeuValLeuValIleSerAlaSerAlaThrHisGlu 20
DB 16 ATGCTCCAAACTCAGCAGTGCTTCTGGTGTGTGTGATCAGTGTCTTGCACACCATGAG 75
QY 21 AlaGluGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
DB 76 GCGAGCAGAAATGACTCTGTGAGCCCCCAGGAAATCCCCAGTGGCGGCCCAAACTCAGCT 135
QY 41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
DB 136 GAAGTGGTTCGTTCCTCAACAGTGCTTACAGGTGCGCTTGGCGGGGCTTTTGCATGCTG 195
QY 61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
DB 196 GAAAACTCCACCTGTGACACAGATGGATGTATGACATCTGTAAATCTCTTGTGTACAGC 255
QY 81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAla 100
DB 256 GCTCTAAATTTGACACTCAGGGAAGAAAGCATTCGTCAAGAGAGAGCTTAAATGTCATGCC 315
QY 101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
DB 316 AACGGGGTCACTCCAAAGGTCTTCTCGCCATTCGGAGGTGCTCCACTTTCCAAAGGATG 375
QY 121 IleAlaGluValGlnGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
DB 376 ATTCTGAGGTGCGAGGAGAGTGTCTACAGCAAGCTGAATGTGTGCGCATGCCAAGCGG 435
QY 141 AsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
DB 436 AACCTTGAGCCATCACTGAGTGTCTCCAGTGTCCCAATCACTTCTCCACAGATATAT 495
QY 161 AsnArgIleValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp 180
DB 496 AACAGACTTGTCCGAAGCCTGTGGAATGTGATGAAGACACAGTCAGCACCAATCAGAGAC 555
QY 181 SerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
DB 556 AGCCTGATGGAGAAATTTGGCCTTAACATGGCCAGCCTCTTCCACATCTCTGCAGACAGAC 615
QY 201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgThrAsnGluProGln 220
DB 616 CACTGTGCCAAACACACACCCAGAGTGACTTCAACAGGAGACGACCAATGAGCGCGAG 675
QY 221 LysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHisIleLys 240
DB 676 AAGCTGAAAGTCTCTCCAGGAACCTCCAGGTGAGGAGGACTCTCCCTCCACATCAAA 735
QY 241 ArgThrSerHisGluSerAla 247
DB 736 CGCACATCCCATGAGAGTGCA 756

RESULT 5
ID AAZ39520 standard; cDNA; 771 BP.
XX
AC AAZ39520;
XX
DT 11-FEB-2000 (first entry)
XX
DE Human corpuscles of stannius polypeptide encoding cDNA.
XX
KW Corpuscles of stannius polypeptide; calcium; inhibition; human; renal;
KW therapeutic; bone; heart disease; hypocalcaemia; osteoporosis; ss.
XX

```


QY 101 AnGlyValThrSerLysValPheLeuAlaIleArgCysSerThrPheGlnArgMet 120
 DB 565 AACGGGGTCACTCCCAAGGCTCTTCCTCGCCATTCGGAGGTGCTCCACITTCACAAAGGATG 624
 QY 121 IleAlaGluValGlnGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
 DB 625 ATTGCTGAGGTGAGGAGAGTGTACAGCAAGCTGAATGTGTGAGCATCGCCAAAGCGG 684
 QY 141 AnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
 DB 685 AACCTGGAAGCATCACTGAGTGTGTCAGCTGCGCCCAATCACTTCTCCAACAGATACATAT 744
 QY 161 AnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp 180
 DB 745 AACAGACTTGTCCGAAGCCTGCTGGAATGTGATGAAGACACAGTCAGCACATCAGAGAC 804
 QY 181 SerLeuMetGlu-LysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAs 200
 DB 805 AGCCTGATGGAGRAAATTNGGGCCTTAACATGGCCAGCCTCTTCCACATCCTGCAGACAGA 864
 QY 200 phiCysAlaGlnThrHisProArgAlaAspPheAsnArgArgThrAsnGluProGlu 220
 DB 865 CCACCTGTGCCCAACACACCCAGAGCTGACTTCAACAGGAGACCAATGAGCCGCA 924
 QY 220 nLysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHisIleIle 240
 DB 925 GAAGCTGAAAGTCTCTCCAGCACTCCGAGGTGAGGAGGACTCTCCCTCCACATCA 984
 QY 240 sArgThrSerHisGluSerAla 247
 DB 985 ACGCATCCCATGAGAGTGCA 1006

RESULT 9
 AAHS5624
 ID AAHS5624 standard; DNA; 585 BP.
 XX
 AC AAHS5624;
 DT 04-SEP-2001 (first entry)
 XX
 DE Human breast tumour protein clone 48987 DNA sequence.
 KW Cytostatic; vaccine; human; breast tumour protein; breast cancer;
 KW gene therapy; ds.
 XX Homo sapiens.
 OS
 PN WO200140269-A2.
 XX
 PD 07-JUN-2001.
 XX
 PF 29-NOV-2000; 2000WO-US32520.
 XX
 PR 30-NOV-1999; 99US-0451651.
 PR 22-FEB-2000; 2000US-0510662.
 PR 10-MAR-2000; 2000US-0523586.
 PR 07-APR-2000; 2000US-0545068.
 PR 15-MAY-2000; 2000US-0571025.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Dillion DC, Day CH, Jiang Y, Houghton RL, Mitcham JL, Wang A;
 XX
 DR WPI; 2001-356154/37.
 XX
 PT Breast tumor polypeptides and the nucleic acids that encode them,
 PT useful for the prevention, diagnosis and treatment of breast cancer -
 XX
 PS Claim 24; Page 168; 221pp; English.
 XX
 CC The present sequence is a human breast tumour protein coding sequence.
 CC This sequence may be used in the prevention, diagnosis and treatment of

CC diseases associated with inappropriate expression of the breast tumour
 CC protein e.g. breast cancer. For example, this sequence may be used to
 CC treat disorders associated with decreased expression by rectifying
 CC mutations or deletions in a patient's genome that affect the activity of
 CC breast tumour protein by expressing inactive proteins or to supplement
 CC the patients own production of the breast tumour protein. Additionally,
 CC the present sequence may be used to produce the breast tumour protein, by
 CC inserting the nucleic acids into a host cell and culturing the cell to
 CC express the protein. The present sequence and its complementary sequences
 CC may also be used as DNA probes in diagnostic assays to detect and
 CC quantitate the presence of similar nucleic acids in samples, and
 CC therefore which patients may be in need of restorative therapy.
 XX
 SQ Sequence 585 BP; 171 A; 163 C; 136 G; 110 T; 5 other;
 Alignment Scores: 7.64e-92 Length: 585
 Pred. No.: 861.00 Matches: 166
 Score: 98.22% Conservative: 0
 Percent Similarity: 98.22% Mismatches: 3
 Best Local Similarity: 67.90% Indels: 0
 Query Match: 22 Gaps: 0
 DB:
 US-09-705-500A-3 (1-247) x AAHS5624 (1-585)
 QY 79 TyrSerAlaAlaLysPheAspThrGlnGlyLysAlaPheValLysSerLeuLysCys 98
 DB 6 TACANCACTGCTAAATTTGACACTNANGAAAGCAATTCGTCAAAGAGAGCTTAAATGTC 65
 QY 99 IleAlaAsnGlyValThrSerLysValPheLeuAlaIleArgCysSerThrPheGln 118
 DB 66 ATCCCAACGGGGTCACTCCCAAGGTCTTCTCCGCCATTCGGAGGTGCTCCACTTTCCAA 125
 QY 119 ArgMetIleAlaGluValGlnGluCysTyrSerLysLeuAsnValCysSerIleAla 138
 DB 126 AGGATGATTGCTGAGGTGCAGAAAGAGTGTACAGCAAGCTGAATGTGTGAGCATGCC 185
 QY 139 LysArgAsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArg 158
 DB 186 AAGCGGAACCTGAAGCCATCACTGAGTGTCTCCAGCTGCCCAATCACTTCTCCAACAGA 245
 QY 159 TyrTyrAsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIle 178
 DB 246 TACTATTAACAGACTTGTCCGAAGCCTGTGGAATGTGTATGAAGACACAGTCAGCAATC 305
 QY 179 ArgAspSerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGln 198
 DB 306 AGAGACAGCTGTATGGAGAAATTTGGGCTTAACATGGCCAGCTTCTCCACATCTCTGAG 365
 QY 199 ThrAspHisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgThrAsnGlu 218
 DB 366 ACAGACCACTGTGCCCAACACACCCAGAGCTGACTTCAACAGGAGACGACCAATCAG 425
 QY 219 ProGlnLysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHis 238
 DB 426 CCGCAGAAGCTGAAAGTCTCTCTCAGGAACCTCCGAGGTGAGGAGGACTCTCCCTCCAC 485
 QY 239 IleLysArgThrSerHisGluSerAla 247
 DB 486 ATCAACGCGCATCCCATGAGAGTGCA 512
 RESULT 10
 AAHS5624
 ID AAHS5624 standard; cDNA; 2191 BP.
 XX
 AC AAHS5624;
 DT 30-NOV-1990 (first entry)
 XX
 DE Sequence encoding Corpuscles of Stannius CS protein precursor.
 KW Corpuscles of Stannius; CS protein; cardiovascular disease;
 KW oedema; heart failure; high blood pressure; ss.

Qy	121	IleAlaGluValGlnGluCysTyrSerIysLeuAsnValCysSerIleAlaLysArg	141
Db	479	ATCTCAGAGGTTTACGAGGAGTGCTATAGCAAACTAGACCTCTGCTCTGTGTTGCCAGAGC	538
Qy	141	AsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyr	160
Db	539	AACCCAGAGGCCATGGGGAGGTGGCCAGGTGCCAGCTTCTCCCAACAGGTACTAC	598
Qy	161	AsnArgLeuValArgSer-LeuLeuGluCysAspGluAspThrValSerThrIleArgAs	180
Db	599	AGCACCTGTGTGCAGAGTACTTCTGACGTGTGATGAGGACACCGTGGAGCAGGTGAGGCG	658
Qy	180	pSerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAs	200
Db	659	CGGTGGTGTGTCCCGCTGGAGCCAGAGATGGGGGTGCTCTTCCAGCTCTCTCCAGACCAA	718
Qy	200	pHisCys 202	
Db	719	GGCCTGC 725	
Qy	RESULT 11		
AAH55616			
ID	AAH55616 standard; DNA; 420 BP.		
XX			
AC	AAH55616;		
XX			
DT	04-SEP-2001 (first entry)		
XX			
DE	Human breast tumour protein clone 47593 DNA sequence.		
XX			
KW	Cytostatic; vaccine; human; breast tumour protein; breast cancer;		
KW	gene therapy; ds.		
XX			
OS	Homo sapiens.		
XX			
PN	W0200140269-A2.		
XX			
PD	07-JUN-2001.		
XX			
PF	29-NOV-2000; 2000WO-US32520.		
XX			
PR	30-NOV-1999; 99US-0451651.		
PR	22-FEB-2000; 2000US-0510662.		
PR	10-MAR-2000; 2000US-0523586.		
PR	07-APR-2000; 2000US-0545068.		
PR	15-MAY-2000; 2000US-0571025.		
XX			
PA	(CORI-) CORIXA CORP.		
XX			
PI	Dillon DC, Day CH, Jiang Y, Houghton RL, Mitcham JL, Wang A;		
XX			
DR	WPI; 2001-356154/37.		
XX			
PT	Breast tumor polypeptides and the nucleic acids that encode them,		
PT	useful for the prevention, diagnosis and treatment of breast cancer -		
XX			
PS	Claim 24; Page 165; 221pp; English.		
XX			
CC	The present sequence is a human breast tumour protein coding sequence.		
CC	This sequence may be used in the prevention, diagnosis and treatment of		
CC	diseases associated with inappropriate expression of the breast tumour		
CC	protein e.g. breast cancer. For example, this sequence may be used to		
CC	treat disorders associated with decreased expression by rectifying		
CC	mutations or deletions in a patient's genome that affect the activity of		
CC	breast tumour protein by expressing inactive proteins or to supplement		
CC	the patients own production of the breast tumour protein. Additionally,		
CC	the present sequence may be used to produce the breast tumour protein, by		
CC	inserting the nucleic acids into a host cell and culturing the cell to		
CC	express the protein. The present sequence and its complementary sequences		
CC	may also be used as DNA probes in diagnostic assays to detect and		
CC	quantitate the presence of similar nucleic acids in samples, and		
CC	therefore which patients may be in need of restorative therapy.		
XX			

SQ Sequence 420 BP; 118 A; 115 C; 101 G; 65 T; 21 other;

Alignment Scores:

Pred. No.: 1.8e-50 Length: 420
Score: 508.00 Matches: 116
Percent Similarity: 82.27% Conservatives: 0
Best Local Similarity: 82.27% Mismatches: 19
Query Match: 40.06% Indels: 6
DB: 22 Gaps: 0

US-09-705-500A-3 (1-247) x AAH55616 (1-420)

QY 85 AspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAlaAsnGlyValThr 104
Db 1 GACACTCAGGAAAGCATNGNCRAANAGAGCTTAAATGTCATGCCAACGGGTACC 60
QY 105 SerLysValPheLeuAlaIleArgCysSerThrPheGlnArgMetIleAlaGluVal 124
Db 61 TCCAAAGGTCTCTCGCCATTGGAGGTCTCCACTTTCCAAAGGATGATTGCTGAGGTG 120
QY 125 GlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArgAsnProGluAla 144
Db 121 CAGGAAGAGTGTACAGCAAGTGAATGTGCCANCATGCCACAGCGNACCNGAGCC 180
QY 145 IleThrGluValGlnLeuProAsnHisPheSerAsnArgTyrTyrAsnArgLeuVal 164
Db 181 ATCACTGAGGTGCTGAGCTGCCAATCACTTCTCCACANATACTATAACAGACTTGN 240
QY 165 ArgSerLeuLeuGluCysAspGluAspThr-ValSerThrIleArg-AspSerLeuMetG 184
Db 241 CGAAGCTGCTGGAATGNGATGAACACACAGGCGCAGCAATCAGGAGACAGCCTGATGG 300
QY 184 LuLysIleGluProAsnMetAla-SerLeuPheHisIleLeu--GlnThrAspHisCysA 203
Db 301 ANAAANTGGGCTTANCATGGCAGGCTTCTCCACATCTCTGNCANGACAGACCACTGTG 360
QY 203 laGlnThrHisProArg-AlaAspPheAsnArgArgThrAsnGluPro 219
Db 361 CCCAAACACCCNCTGAGCTGACTTNNACAGGAGCAGCACNAAGAGGCC 411

RESULT 12

ABAS1055/c

ID ABAS1055 standard; DNA; 219 BP.

XX AC ABAS1055;

XX DT 01-FEB-2002 (first entry)

XX DE Human breast cell single exon nucleic acid probe #9750.

XX KW Human; microarray; single exon probe; gene expression; breast;

XX OS Homo sapiens.

XX PN WO200157271-A2.

XX PD 09-AUG-2001.

XX PF 30-JAN-2001; 2001WO-US00662.

XX PR 04-FEB-2000; 2000US-0180312.

XX PR 26-MAY-2000; 2000US-0207456.

XX PR 30-JUN-2000; 2000US-0608408.

XX PR 03-AUG-2000; 2000US-0632366.

XX PR 21-SEP-2000; 2000US-0234687.

XX PR 27-SEP-2000; 2000US-0236359.

XX PR 04-OCT-2000; 2000GB-0024263.

XX PA (MOLE-) MOLECULAR DYNAMICS INC.

XX PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX XX

DR WPI; 2001-496933/54.

XX New spatially-addressable set of single exon nucleic acid probes,

PT useful for measuring gene expression in sample derived from human

PT breast, comprises number of single exon nucleic acid probes

XX Claim 4; SEQ ID NO 9750; 327pp + sequence listing; English.

PS The invention relates to a spatially-addressable set of single exon

CC nucleic acid probes for measuring gene expression in a sample derived

CC from human breast and BT 474 cells. The method involves contacting

CC the probes with a collection of detectably labelled nucleic acids

CC derived from mRNA of human breast, and then measuring the label

CC bound to each probe of the microarray. The probes are useful for

CC verifying the expression of regions of genomic DNA predicted to

CC encode proteins. They are useful for gene discovery, and for

CC determining predisposition and/or prognosing breast disease. Gene

CC expression analysis is useful for assessing the toxicity of chemical

CC agents on cells. The microarray of this invention presents a far greater

CC diversity of probes for measuring gene expression, with far less bias

CC than expressed sequence tag microarrays. The method is suitable for

CC rapid production of functional information from genomic sequence. The

CC present sequence is a single exon nucleic acid probe of the invention.

CC Note: The sequence data for this patent did not form part of the

CC printed specification, but was obtained in electronic format directly

CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 219 BP; 43 A; 55 C; 60 G; 61 T; 0 other;

Alignment Scores:

Pred. No.: 1.25e-34 Length: 219

Score: 370.00 Matches: 72

Percent Similarity: 100.00% Conservatives: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 29.18% Indels: 0

DB: 22 Gaps: 0

US-09-705-500A-3 (1-247) x ABAS1055 (1-219)

QY 88 GlyLysAlaPheValLysGluSerLeuLysCysIleAlaAsnGlyValThrSerLysVal 107

Db 219 GGAAGAGCATTCGTCAAAGAGAGAGCTTAAATGTCATGCCAACGGGTCCCTCAAGGTC 160

QY 108 PheLeuAlaIleArgCysSerThrPheGlnArgMetIleAlaGluValGlnGlu 127

Db 159 TTCCTGCCATTCCGAGGTGCTCCACTTCCAAAGGATGATTGCTGAGGTCAGGAAGAG 100

QY 128 CysTyrSerLysLeuAsnValCysSerIleAlaLysArgAsnProGluAlaIleThrGlu 147

Db 99 TGCCTACAGCAAGCTGAATGTGTGAGCATGCCAACGGGAACCCCTGAAGCCATCACTGAG 40

QY 148 ValValGlnLeuProAsnHisPheSerAsnArgTyr 159

Db 39 GTCGTGAGGTGCCCCAATCACTTCTCCAAACAGGTAC 4

RESULT 13

ABAS1055/c

ID ABAS1055 standard; DNA; 219 BP.

XX AC ABAS1055;

XX DT 01-FEB-2002 (first entry)

XX DE Human foetal liver single exon nucleic acid probe #17350.

XX KW Human; foetal liver; gene expression; single exon nucleic acid probe; ss.

XX OS Homo sapiens.

XX PN WO200157277-A2.

XX PD 09-AUG-2001.

XX XX

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PF 30-JAN-2001; 2001WO-US00669.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-483447/52.
XX
PT Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human fetal liver -
XX
XX
PS Claim 4; SEQ ID NO 17350; 639pp + sequence listing; English.
XX
CC The invention relates to a single exon nucleic acid probe for
CC measuring human gene expression in a sample derived from human foetal
CC liver. The single exon nucleic acid probes may be used for predicting,
CC measuring and displaying gene expression in samples derived from human
CC fetal liver. The present sequence is a single exon nucleic acid
CC probe of the invention.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 219 BP; 43 A; 55 C; 60 G; 61 T; 0 other;

Alignment Scores:
Pred. No.: 1-25e-34 Length: 219
Score: 370.00 Matches: 72
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 29.18% Indels: 0
DB: 22 Gaps: 0

US-09-705-500A-3 (1-247) x ABA69045 (1-219)
QY 88 GlyLysAlaPheValLysGluSerLeuLysCysIleAlaAsnGlyValThrSerLysVal 107
Db 219 GGAAGAGCATTCGTCGCAAGAGAGCTTAAATGTCATCGCCACGCGGTCACTCCCAAGGTC 160
QY 108 PheLeuAlaIleArgArgCysSerThrPheGlnArgMetIleAlaGluValGlnGlu 127
Db 159 TTCCTCGCCATTCGGAGGTGCTCCACTTTCCAAAGGATGATTGCTGAGGTGCGAGAGAG 100
QY 128 CysTyrSerLysLeuAsnValCysSerIleAlaLysArgAsnProGluAlaIleThrGlu 147
Db 99 TGCTACAGCAAGCTGAATGTGTGAGCATCGCCACGCGAACCTTGAAGCCATCACTGAG 40
QY 148 ValValGlnLeuProAsnHisPheSerAsnArgTyr 159
Db 39 GTCGTCCAGCTGCCCAATCACTTCTCCCAACAGGTAC 4

RESULT 14
ABA35989/c
ID ABA35989 standard; DNA; 219 BP.
XX
XX ABA35989;
XX
XX 23-JAN-2002 (first entry)
DE
DE Probe #14455 for gene expression analysis in human heart cell sample.
KW Human; gene expression; heart; microarray; vascular system; probe;
KW cardiovascular disease; hypertension; cardiac arrhythmia;
KW congenital heart disease; ss.
XX

OS Homo sapiens.
XX
PN WO200157274-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00666.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-488899/53.
XX
PT Single exon nucleic acid probes for analyzing gene expression in human
PT hearts -
XX
PS Claim 4; SEQ ID No 14455; 530pp; English.
XX
CC The present invention relates to single exon nucleic acid probes for
CC measuring human gene expression in a sample derived from human heart. The
CC present sequence is one such probe. The probes may be used for
CC predicting, measuring and displaying gene expression in samples derived
CC from the human heart via microarrays. By measuring gene expression, the
CC probes are useful for predicting, diagnosing, grading, staging,
CC monitoring and prognosing diseases of the human heart and vascular system
CC e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
CC congenital heart disease.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 219 BP; 43 A; 55 C; 60 G; 61 T; 0 other;

Alignment Scores:
Pred. No.: 1.25e-34 Length: 219
Score: 370.00 Matches: 72
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 29.18% Indels: 0
DB: 22 Gaps: 0

US-09-705-500A-3 (1-247) x ABA35989 (1-219)
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QY 108 PheLeuAlaIleArgArgCysSerThrPheGlnArgMetIleAlaGluValGlnGlu 127
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QY 128 CysTyrSerLysLeuAsnValCysSerIleAlaLysArgAsnProGluAlaIleThrGlu 147
Db 99 TGCTACAGCAAGCTGAATGTGTGAGCATCGCCACGCGAACCTTGAAGCCATCACTGAG 40
QY 148 ValValGlnLeuProAsnHisPheSerAsnArgTyr 159
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ID ABA17358 standard; DNA; 219 BP.
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XX AAK17358;
XX
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Search completed: June 12, 2003, 20:16:40
Job time : 226 secs

[illegible]

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 12, 2003, 20:12:24 ; Search time 67 Seconds
(without alignments)
1130.584 Million cell updates/sec

Title: US-09-705-500A-3

Perfect score: 1268

Sequence: 1 MLQNSAVLLVLVISATHE.....NLRGEDSPSHKRTSHESA 247

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
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-FGAEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DEEXT=7

Database : Issued Patents NA:
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5: /cgn2_6/ptodata/2/ina/PTCUS COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1268	100.0	771	2	US-08-208-005C-1
2	1268	100.0	771	2	US-09-038-597A-1
3	1268	100.0	771	2	US-08-431-117A-1
4	354.5	28.0	888	3	US-08-831-132-13
5	354.5	28.0	888	4	US-09-416-150-13
6	354	27.9	906	3	US-08-831-132-1
7	354	27.9	906	4	US-09-416-150-1
8	352	27.8	892	2	US-08-460-529B-1
9	93.5	7.4	30549	4	US-09-134-001C-322
10	90	7.1	1384	4	US-09-227-357-142
11	85.5	6.7	1971	4	US-09-134-001C-1485
12	84	6.6	10136	1	US-08-353-700-2

13	84	6.6	10136	5	PCT-US95-16216-2	Sequence 2, Appli
14	83	6.5	1254	4	US-09-134-001C-973	Sequence 973, App
15	82	6.5	1089	4	US-09-134-001C-1833	Sequence 1833, Ap
c 16	82	6.5	441529	4	US-09-103-840A-1	Sequence 1, Appli
17	81	6.4	2160	2	US-08-840-236-2	Sequence 2, Appli
18	81	6.4	2160	2	US-08-840-236-5	Sequence 5, Appli
19	81	6.4	2160	2	US-08-505-448A-2	Sequence 2, Appli
20	81	6.4	2160	2	US-08-505-448A-5	Sequence 5, Appli
21	81	6.4	3467	4	US-09-298-924-3	Sequence 3, Appli
c 22	80	6.3	4403765	4	US-09-103-840A-2	Sequence 2, Appli
23	79.5	6.3	2347	1	US-08-145-681-3	Sequence 3, Appli
24	79.5	6.3	2347	1	US-08-453-703-3	Sequence 3, Appli
25	79.5	6.3	2347	2	US-08-456-106-3	Sequence 3, Appli
26	79.5	6.3	2347	3	US-08-456-108-3	Sequence 3, Appli
27	79.5	6.3	2347	4	US-09-265-577-3	Sequence 3, Appli
c 28	78.5	6.2	1447	4	US-09-484-970B-121	Sequence 121, App
c 29	78	6.2	18475	4	US-08-961-527-38	Sequence 38, Appl
c 30	77	6.1	714	4	US-09-221-017B-1030	Sequence 1030, Ap
31	76.5	6.0	1391	4	US-09-615-192A-352	Sequence 352, App
32	76.5	6.0	3572	2	US-08-713-815A-2	Sequence 2, Appli
c 33	76	6.0	1461	2	US-08-578-516-1	Sequence 1, Appli
34	75.5	6.0	1479	2	US-08-686-599A-4	Sequence 4, Appli
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36	75	5.9	2840	5	PCT-US93-06251-64	Sequence 64, Appli
37	75	5.9	5816	4	US-09-220-641-4	Sequence 4, Appli
c 38	75	5.9	11091	4	US-09-134-001C-2243	Sequence 2243, Ap
c 39	75	5.9	12508	4	US-09-655-270A-1	Sequence 1, Appli
c 40	75	5.9	12523	4	US-09-651-941-1	Sequence 1, Appli
c 41	75	5.9	12523	4	US-09-955-597-1	Sequence 1, Appli
42	74.5	5.9	1602	2	US-08-770-544-3	Sequence 3, Appli
43	74.5	5.9	2259	6	S185254-3	Patent No. S185254
44	74.5	5.9	3515	4	US-09-221-017B-824	Sequence 824, App
45	74	5.8	1026	4	US-09-134-001C-1431	Sequence 1431, Ap

ALIGNMENTS

RESULT 1
US-08-208-005C-1
; Sequence 1, Application US/08208005C
; Patent No. 5837498
; GENERAL INFORMATION:
; APPLICANT: OLSEN, ET AL.
; TITLE OF INVENTION: Corpuscles of Stannius Protein, Stannioalcin
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/208,005C
; FILING DATE: 8 MARCH 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: FERRARO, GREGORY D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-78
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 1:


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Db 316 AACGGGGTCACTCCAAAGGCTTCTCGCCATTCGGAGGTGCTCCACCTTCCAAAGGATG 375
Qy 121 IleAlaGluValGlnGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
Db 376 ATTGCTGAGGTGCAGGAAGAGTGCTACAGCAAGCTGATGTGTGAGCATGCCAAGCGG 435
Qy 141 AsnProGluAlaIleThrGluValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
Db 436 AACCTGAAGCCATCACTGAGGTGCTCCAGTGCCTCAATCACTTCCCAACAGATACAT 495
Qy 161 AsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp 180
Db 496 AACAGACTTGTCGGAAGCTGCTGGAATGTGATGAAGACACAGTCAGCAATCAGAC 555
Qy 181 SerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
Db 556 AGCCTGATGGAGAAATTTGGGCTTAACATGGCCAGCCTCTCCACATCCTCGACAGAC 615
Qy 201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgThrAsnGluProGln 220
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Qy 221 LysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHisIleLys 240
Db 676 AAGCTGAAGTCTCTCCTCAGGAACCTCCGAGGTGAGGAGGACTCTCCCTCCACATCAA 735
Qy 241 ArgThrSerHisGluSerAla 247
Db 736 CGCACATCCCATGAGATGCA 756

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RESULT 3

US-08-431-117A-1
; Sequence 1, Application US/08431117A
; Patent No. 5994301

GENERAL INFORMATION:

; APPLICANT: OLSEN, ET AL.
; TITLE OF INVENTION: Corpuscles of Stannius Protein, Stanniocalcin

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,

; ADDRESSEE: CECCHI, STEWART & OLSTEIN

; STREET: 6 BECKER FARM ROAD

; CITY: ROSELAND

; STATE: NEW JERSEY

; COUNTRY: USA

; ZIP: 07068

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 INCH DISKETTE

; COMPUTER: IBM PS/2

; OPERATING SYSTEM: MS-DOS

; SOFTWARE: WORD PERFECT 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/431,117A

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/208,005

; FILING DATE: 8 MARCH 1994

; ATTORNEY/AGENT INFORMATION:

; NAME: FERRARO, GREGORY D.

; REGISTRATION NUMBER: 36,134

; REFERENCE/DOCKET NUMBER: 325800-296

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 201-994-1700

; TELEFAX: 201-994-1744

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 771 BASE PAIRS

; TYPE: NUCLEIC ACID

; STRANDEDNESS: SINGLE

; TOPOLOGY: LINEAR

; MOLECULE TYPE: CDNA

US-08-431-117A-1

Alignment Scores:

Pred. No.: 3.15e-152 Length: 771
Score: 1268.00 Matches: 247
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-705-500A-3 (1-247) x US-08-431-117A-1 (1-771)

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Db 76 GCGGAGCAGATGACTCTGTGAGCCCGAGGAAATCCCGAGTGGCGGCCCAAACTCAGCT 135
Qy 41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
Db 136 GAAGTGGTTCGTTCCCTCAACAGTGTCTACAGTTCGGCTCGGGGCTTTTGCATGCTG 195
Qy 61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
Db 196 GAAAACTCCACCTGTGACACAGATGGGATGTATGACATCTGTAATCTCTTGTACAGC 255
Qy 81 AlaAlaLysPheAspThrGlnGlyAlaPheValLysGluSerLeuLysCysIleAla 100
Db 256 GCTGCTAAATTTGACACTCAGGGGAAAGCATTCTGCAAGAGAGCTTAAATATGATCGCC 315
Qy 101 AsnGlyValThrSerLysValPheLeuAlaIleArgCysSerThrPheGlnArgMet 120
Db 316 AACGGGTGCTCCCAAGGCTTCTCGCCATTCGGAGGTGCTCCACTTTCCAAAGGATG 375
Qy 121 IleAlaGluValGlnGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
Db 376 ATTGCTGAGGTGCAGGAAGAGTGCTACAGCAAGCTGAATGTGTGAGCATGCCAAGCGG 435
Qy 141 AsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
Db 436 AACCTGAAGCCATCACTGAGGTGCTCCAGTGCCTCAATCACTTCTCCACAGATACAT 495
Qy 161 AsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp 180
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Db 556 AGCCTGATGGAGAAATTTGGGCTTAACATGGCCAGCCTCTTCCACATCCTCGACAGAC 615
Qy 201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgThrAsnGluProGln 220
Db 616 CACTGTGCCCAACACACCCAGAGCTGACTTCAACAGGAGACGACCAATGAGCGCGAG 675
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RESULT 4

US-08-831-132-13

; Sequence 13, Application US/088311132

; Patent No. 6008322

; GENERAL INFORMATION:

; APPLICANT: Kuestner, Rolf E.

; APPLICANT: Konkin, Darrell C.

; APPLICANT: Lok, Si

; APPLICANT: Buddle, Michele

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; APPLICANT: Downey, William
; TITLE OF INVENTION: STANNIOCALCIN-2
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/831,132
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A.
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 96-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6672
; TELEFAX: 206-442-6678
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 888 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 1..72
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 73..888
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..888
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; US-08-831-132-13
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; Alignment Scores:
; Pred. No.: 9,86e-36 Length: 888
; Score: 354.50 Matches: 85
; Percent Similarity: 48.51% Conservative: 45
; Best Local Similarity: 31.72% Mismatches: 109
; Query Match: 27.96% Indels: 29
; DB: 3 Gaps: 5
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; QY 27 ValSerPro-----ArgLysSerArgValAla 36
; DB 82 ACGAACCTCGGAGAGTCCCAAGACAGAGGAGCTCCGACAGAGAAAGCGCGTGTGTCCTG 141
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; QY 37 GlnAsnSerAlaGluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAla 56
; DB 142 CAGACACAGCGGAGATCCAGCAGCTGTTGGTCATGCGGGGAGCGTGGCTGTGGTG 201
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; QY 57 PheAlaCysLeuGluAsnSerThrCysAspThrAspGlyMetTyrAspLeuCysLysSer 76
; DB 202 TTGAGTGTTCGAGAACAACTCTTGTAATCCAGGGTTTACATGGGATTTCATGACG 261
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; QY 77 PheLeuTyrSerAlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeu 96
; DB 262 TTTCGACACAGCGTGGAAATTCGATGCCAGGGAAAGTTCATTCATCAAGGATGCCCTG 321

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; QY 97 LysCysIleAlaAsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThr 116
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; QY 117 PheGlnArgMetIleAlaGluValGlnGluCysTyrSerLysLeuAsnValCysSer 136
; DB 382 ATTAGGAAATGGTTTCCAGTTGCAGAGGAATCTATCTGAAGCATGACCTGTCTCC 441
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; QY 137 IleAlaLysArgAsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSer 156
; DB 442 GCAGCCAGGAGAACGTCGGTGTGATTGTGGAGATGATTTCATTCAAGGATCTCTGCTG 501
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; QY 157 AsnArgTyrAsnArgLeuValArgSerLeuGluCysAspGluAspThrValSer 176
; DB 502 CATGAGCCCTATGTGGACCTTGTGAACCTGTGCTGACCTGCGGGAGATGTGAAGGAG 561
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; QY 177 ThrLeuArgAspSerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIle 196
; DB 562 GCAGTCACCCGCGAGCTCCAGGCTCAGTGTGAACAGAGCTGGGGAGGCTCTGTCTCCATC 621
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; QY 197 Leu-----GlnThrAspHisCysAlaGlnThrHis----- 206
; DB 622 CTGAGTTTCTCACCTCCAATATACAGAGACCTCCACGCGAGCGCCAGAGCATCAGCCC 681
;
; QY 207 -----ProArgAlaAspPheAsnArgArgThrAsnGluProGlnLysLeuLysVal 224
; DB 682 CTGGCAGACAGGCTCAGCTCTCCAGGCTCACCACCGGACAGACATCACCTAACA 741
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; QY 225 LeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHisIleLys----- 240
; DB 742 GCCAACAGAGGTGCCAAGGTGAGCGAGGAGCAAAAGCCACCGCAATGCCCATCTCGA 801
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; QY 241 ---ArgThrSerHisGluSerAla 247
; DB 802 GGCAGAACCCGTGGCCAGAGCGCT 825
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; RESULT 5
; US-09-416-150-13
; Sequence 13, Application US/09416150
; Patent No. 6171822
; GENERAL INFORMATION:
; APPLICANT: Kuestner, Rolf E.
; Conklin, Darrell C.
; Lok, Si
; Buddle, Michele
; Downey, William
; TITLE OF INVENTION: STANNIOCALCIN-2
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc. East
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/416,150
; FILING DATE: 11-Oct-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/831,132
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A.
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 96-01
; TELECOMMUNICATION INFORMATION:

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; TELEPHONE: 206-442-6672
; TELEFAX: 206-442-6678
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 888 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 1..72
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 73..888
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..888
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-416-150-13

Alignment Scores:
Pred. No.: 9,86e-36 Length: 888
Score: 354.50 Matches: 85
Percent Similarity: 48.51% Conservative: 45
Best Local Similarity: 31.72% Mismatches: 109
Query Match: 27.96% Indels: 29
DB: 4 Gaps: 5

US-09-705-500A-3 (1-247) x US-09-416-150-13 (1-888)
QY 7 ValLeuLeuValValValSerAlaSerAlaThrHisGluAlaGluAsnAspSer 26
Db 28 GTGACCTGGCTTGGTGTGTT-----GCCACCTTGGACCGCGGAGGACGACGCC 81
QY 27 ValSerPro-----ArgLysSerArgValAlaAla 36
Db 82 AGCAACCTCCGGAAGGTCCCAAGACAGGAGCTCGACAGAGAAAGGCGCTGTGCTCGT 141
QY 37 GlnAsnSerAlaGluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAla 56
Db 142 CAGAACACAGCGGAGATCCAGCAGCTGTTTGGTCAATGCCGGGAGCGTGGCTGTGTGTG 201
QY 57 PheAlaCysLeuGluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSer 76
Db 202 TTTGAGTGTTCGAGAACAACTCTGTGAAATCCAGGTTTACATGGGATTTGCATGACG 261
QY 77 PheLeuTyrSerAlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeu 96
Db 262 TTTCTGCACACGCTGGGAAATTCGATCCCAAGGAAAGTCAATCATCAAGGATGCCCTG 321
QY 97 LysCysIleAlaAsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThr 116
Db 322 AGGTGCAGGCCATCGCTCGCTGCTATAAATTTGGCTGCATCAGCAGGAAGTGTCCAGCA 381
QY 117 PheGlnArgMetIleAlaGluValGlnGluCysTyrSerLysLeuAsnValCysSer 136
Db 382 ATTAGCGAAATGGTTTTCCAGTTGCAGGGAATGCTATCTGAACATGACCTGTGTCTCC 441
QY 137 IleAlaLysArgAsnProGluValIleThrGluValValGlnLeuProAsnHisPheSer 156
Db 442 GCAGCCAGGAGAACGTCGGTGTGATTGTGGAGATGATTTCATTCAAGGATCTCTCTGTG 501
QY 157 AsnArgTyrTyrAsnArgLysValArgSerLeuLeuGluCysAspGluAspThrValSer 176
Db 502 CATGAGCCCTATGTGGACCTGTGTGAACCTGTGTGCTGCTGCTGCGGGAAGATGTGAGGAG 561
QY 177 ThrIleArgAspSerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIle 196
Db 562 GCAGTCCACCGCGGCTCCAGGCTCAGTGTGTAACAGAGCTGGGAGGCGCTCTGTCTCCATC 621
QY 197 Leu-----GlnThrAspHisCysAlaGlnThrHis----- 206
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Db 622 CTGAGTTTCTGCACCTCCATATATACAGAGACCTCCACGGGAGCCGCCAGACATCAGCCC 681
QY 207 -----ProArgAlaAspPheAsnArgArgThrAsnGluProGlnLysLeuLysVal 224
;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 888 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 1..72
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 73..888
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..906
; US-08-831-132-1

Alignment Scores:
Pred. No.: 1.18e-35 Length: 906
Score: 354.00 Matches: 82
Percent Similarity: 52.32% Conservative: 42
Best Local Similarity: 34.60% Mismatches: 102
Query Match: 27.92% Indels: 12

US-08-831-132-1
; Sequence 1, Application US/08831132
; Patent No. 6008322
; GENERAL INFORMATION:
; APPLICANT: Kuestner, Rolf E.
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Lok, Si
; APPLICANT: Buddle, Michele
; APPLICANT: Downey, William
; TITLE OF INVENTION: STANNIOCALCIN-2
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/831,132
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A.
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 96-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6672
; TELEFAX: 206-442-6678
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 906 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 1..72
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 73..906
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..906
; US-08-831-132-1

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DB: 3 3 Gaps: 4
US-09-705-500A-3 (1-247) x US-08-831-132-1 (1-906)
QY 9 LeuValLeuValIleSer-----AlaSerAlaThrHisGluAla 21
DB 34 CTGGCTTTGGTGTGGCCACCTTTGACCGGGGGGAGCCGACCGCCACCAACCCACCC 93
QY 22 Glu---GlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
DB 94 GAGGTCTCCAGACAGAGAGCTCCAGCAGAAAGCCGCTTCCTGCGAGAAATGACAGG 153
QY 41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
DB 154 GAGATCCAGCACTGTTTGTCAACGCTGGCGATGGGGTGTGGCTGTTGAATGTTTC 213
QY 61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
DB 214 GAGAACAACTCTGTGAGATTCCGGGCTTACATGGGATTTCATGATCTTTCTGCACAA 273
QY 81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLysCysIleAla 100
DB 274 GCTGGAATAATTTGATGCCAGGCAAGTCATTATCAAGACGCTTGAATGTAAGGCC 333
QY 101 AsnGlyValThrSerLysValPheLeuAlaIleArgCysSerThrPheGlnArgMet 120
DB 334 CACGCTCTGCGGCACAGGTTTCGGCTGCATAGCCGGAAGTCCCGCCATCAGGAAATG 393
QY 121 IleAlaGluValGlnGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
DB 394 GTGTCCAGTTGCAGCGGAATGCTACCTCAAGCAGCAGCTGTGCGGGTGTGCGGAGG 453
QY 141 AsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyr 160
DB 454 AACCCCGGGTATGATGAGATGATCCATTTCAGGAGCTTGTGCTGCAGCAACCTTAC 513
QY 161 AsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp 180
DB 514 GTGGACCTCGTGAACCTGTGTGACCTGTGGGAGGAGGTGAAGAGGCCATCACCAC 573
QY 181 SerLeuMetGluLysIleGlyProMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
DB 574 AGCGTGCAGGTTTCAGTGTGAGCAGAACTGGGGAAGCCTGTGCTCCATCTTG-----AGC 627
QY 201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgArgThrAsnGluProGln 220
DB 628 TTCTGCACCTCGGC-CATCCAGAGCTCCACGGGGCCCCCGAGCGCCAGCCACAGT 686
QY 221 LysLeuLysValLeuLeuArgAsn---LeuArgGlyGluGluAspSerPro 236
DB 687 GGACAGAACCAAGCTCTCCAGGGCCCAACACCGGGAAGCAGGACATCACCT 737

RESULT 7
US-09-416-150-1
; Sequence 1, Application US/09416150
; Patent No. 6171822
; GENERAL INFORMATION:
; APPLICANT: Kuestner, Rolf E.
; Conklin, Darrell C.
; Lok, Si
; Buddle, Michele
; Downey, William
; TITLE OF INVENTION: STANNIOCALCIN-2
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/416,150
; FILING DATE: 11-Oct-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/831,132
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A.
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 96-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6672
; TELEFAX: 206-442-6678
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 906 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 1..72
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 73..906
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..906
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-416-150-1

Alignment Scores:
Pred. No.: 1,18e-35 Length: 906
Score: 354.00 Matches: 82
Percent Similarity: 52.32% Conservative: 42
Best Local Similarity: 34.60% Mismatches: 102
Query Match: 27.92% Indels: 12
DB: 4 Gaps: 4

US-09-705-500A-3 (1-247) x US-09-416-150-1 (1-906)
QY 9 LeuValLeuValIleSer-----AlaSerAlaThrHisGluAla 21
DB 34 CTGGCTTTGGTGTGGCCACCTTTGACCGGGGGGAGCCGACCGCCACCAACCCACCC 93
QY 22 Glu---GlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
DB 94 GAGGTCTCCAGACAGAGAGCTCCAGCAGAAAGCCGCTTCCTGCGAGAAATGACAGG 153
QY 41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
DB 154 GAGATCCAGCACTGTTTGTCAACGCTGGCGATGGGGTGTGGCTGTTGAATGTTTC 213
QY 61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
DB 214 GAGAACAACTCTGTGAGATTTCGGGCTTACATGGGATTTCATGATCTTTCTGCACAA 273
QY 81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLysCysIleAla 100
DB 274 GCTGGAATAATTTGATGCCAGGCAAGTCATTATCAAGACGCTTGAATGTAAGGCC 333
QY 101 AsnGlyValThrSerLysValPheLeuAlaIleArgCysSerThrPheGlnArgMet 120
DB 334 CACGCTCTGCGGCACAGGTTTCGGCTGCATAGCCGGAAGTCCCGCCATCAGGAAATG 393
QY 121 IleAlaGluValGlnGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
DB 394 GTGTCCAGTTGCAGCGGAATGCTACCTCAAGCAGCAGCTGTGCGGGTGTGCGGAGG 453

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QY 141 AsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
 DB 454 AACACCCGGGTGATAGTGGAGATGATCCATTTCAAGGACTTCTGTCGACGAACCTTAC 513
 QY 161 AsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp 180
 DB 514 GTGGACCTCGTGAACCTGCTGCTGACCTGTGGGAGGAGGTGAAGAGGCCATCACCCAC 573
 QY 181 SerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
 DB 574 AGCGTCAGGTTCACTGTCAGCAGCAACTGGGGAAGCCTGTGCTCCATCTTG-----AGC 627
 QY 201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgThrAsnGluProGln 220
 DB 628 TTCTGCACCTCGGC-CATCCAGAAGCCTCCACGGCGCCCGCCGAGCGCCAGCCCGAGGT 686
 QY 221 LysLeuLysValLeuLeuArgAsn---LeuArgGlyGluGluAspSerPro 236
 DB 687 GGACAGAACCAAGTCTTCAGGGGCCACACCGGGGAAGCAGGACATCACCT 737

RESULT 8

US-08-460-529B-1
 ; Sequence 1, Application US/08460529B
 ; Patent No. 5994103

GENERAL INFORMATION:

; APPLICANT: OLSEN, ET AL.
 ; TITLE OF INVENTION: Human Stanniocalcin-alpha
 ; NUMBER OF SEQUENCES: 10
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSES: CARELLA, BYRNE, BAIN, GILFILLAN,
 ; ADDRESSES: CECCHI, STEWART & OLSTEIN
 ; STREET: 6 BECKER FARM ROAD
 ; CITY: ROSELAND
 ; STATE: NEW JERSEY
 ; COUNTRY: USA
 ; ZIP: 07068

COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 INCH DISKETTE
 ; COMPUTER: IBM PS/2
 ; OPERATING SYSTEM: MS-DOS
 ; SOFTWARE: WORD PERFECT 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/460,529B
 ; FILING DATE: June 2, 1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US94/13206
 ; FILING DATE: 10 NOV 1994

ATTORNEY/AGENT INFORMATION:

; NAME: MULLINS, J.G.
 ; REGISTRATION NUMBER: 33,073
 ; REFERENCE/DOCKET NUMBER: 325800-334 (PF143)
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 201-994-1700
 ; TELEFAX: 201-994-1744

INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 892 BASE PAIRS
 ; TYPE: NUCLEIC ACID
 ; STRANDEDNESS: SINGLE
 ; TOPOLOGY: LINEAR
 ; MOLECULE TYPE: cDNA
 ; US-08-460-529B-1

Alignment Scores:

Pred. No.: 2,07e-35 Length: 892
 Score: 352.00 Matches: 81
 Percent Similarity: 52.94% Conservative: 45
 Best Local Similarity: 34.03% Mismatches: 101
 Query Match: 27.76% Indels: 12
 DB: 2 Gaps: 4

US-09-705-500A-3 (1-247) x US-08-460-529B-1 (1-892)

QY 9 LeuValLeuValIleSer-----AlaSerAlaThrHisGluAla 21
 DB 115 CTGGCTTTGGTGTGGCCACCTTTGACCCGGCGGGGACCGGACCCACCAACCCACCC 174
 QY 22 Glu---GlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
 DB 175 GAGGTCTCCCAAGACAGGAGCTCCACGACAGAAAGCCGCTGTCCCTCAGAATAACAGCG 234
 QY 41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
 DB 235 GAGATCCAGCACTGTTGGTCAAGCTGCGCATGTGGGGTGTGGCTGTTGAATGTTTC 294
 QY 61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
 DB 295 GAGAACAACTCTTGAGATTCCGGGCTTACATGGGATTTGCATGACTTTCTGCACAAC 354
 QY 81 AlaAlaLysPheAspThrGlnGlyAlaPheValLysGluSerLeuLysCysIleAla 100
 DB 355 GCTGGAATAATTGATGCCCGGCAAGTCATTATCAAGACGCTTGAAATGTAAAGGCC 414
 QY 101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
 DB 415 CACGCTCTCGGCGCACAGTTCGGCTGTCATAAGCCGGAAGTCCCGGCCCATCAGGAAATG 474
 QY 121 IleAlaGluValGlnGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
 DB 475 GTGTCCCACTGGAGCGGGAATGCTACCTCAAGCACGACCTGTGGCGGCTGCCCAGGAG 534
 QY 141 AsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
 DB 535 AACACCCGGGTGATAGTGGAGATGATCCATTTCAAGGACTTGTCTGCTCAGCAACCTTAC 594
 QY 161 AsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp 180
 DB 595 GTGGACCTCGTGAACCTGCTGCTGACCTGGGAGGAGGTGAAGAGGCCATCACCCAC 654
 QY 181 SerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
 DB 655 AGCGTCAGGTTCACTGTCAGCAGCAACTGGGGAAGCCTGTGCTCCATCTTG-----AGC 708
 QY 201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgThrAsnGluProGln 220
 DB 709 TTCTGCACCTCGGA-CATCCAGAAGCCTCCACGGCGCCCGCCGAGCGCCAGCCAGGT 767
 QY 221 LysLeuLysValLeuLeuArgAsn---LeuArgGlyGluGluAspSerProSer 237
 DB 768 GGACAGAACCAAGTCTTCAGGGGCCACACCGGGGAAGAGGACATCACCTCC 821

RESULT 9

US-09-134-001C-322
 ; Sequence 322, Application US/09134001C
 ; Patent No. 6380370

GENERAL INFORMATION:

; APPLICANT: Lynn Doucette-Stamm et al
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
 ; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: GTC-007
 ; CURRENT APPLICATION NUMBER: US/09/134,001C
 ; CURRENT FILING DATE: 1998-08-13
 ; PRIOR APPLICATION NUMBER: US 60/064,964
 ; PRIOR FILING DATE: 1997-11-08
 ; PRIOR APPLICATION NUMBER: US 60/055,779
 ; PRIOR FILING DATE: 1997-08-14
 ; NUMBER OF SEQ ID NOS: 5674
 ; SEQ ID NO 322
 ; LENGTH: 30549
 ; TYPE: DNA

; ORGANISM: Staphylococcus epidermidis

US-09-134-001C-322

Alignment Scores:

QY 85 pThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAlaAsnGlyValThrSe 105
Db 431 TCATGAACCTTCAA-----GTCAAGAGTCAACAAGTAAATTTCCAGGAAGCAACTGAA 484
QY 105 r-----LysValPheLeuAlaIleArgArgCysSerThrPheG1 118
Db 485 TTCAGGCAAAAAAATAAGAAACTGGAACAGCAACTTAAAGGTGTAAATCTGAGCT 544
QY 118 nArgMetIleAlaGluValGlnGluCysTyrSerLysLeuAsnValCysSerIleAl 138
Db 545 TGAAGAAGCCCAACAGCTGCGCAGTCTCTCTGAATCCATGCAAT-----599
QY 138 aLysArgAsnProGluAlaIleThrGluValGlnLeuProAsnHisPhe-----Se 156
Db 600 -----ACACCAAAAAATTTTACAACTCCACTAACCAACCAAGTCAATATTAAGTGG 652
QY 156 rAsnArgTyr-----TyrAsnArgLeuVal-----ArgSerLeuLe 168
Db 653 TTCCAAGTATGAAGATCTAAAGAAATAATAAAGAGGTTGAAGAACGAAAGAAAT 712
QY 168 uGluCysAspGluAspThrValSerThrIleArgAspSerLeuMetGluLysIleGlyPr 188
Db 713 AGAGGCAGAG-----722
QY 188 oAsnMetAlaSerLeuPheHisIleLeuGlnThrAspHisCysAlaGlnThrHisProAr 208
Db 723 -----GTTAAAGCCTTGCAGGCTAAAAAAGCAAGCCAGACTCTTCCACA 766
QY 208 gAlaAspPheAsnArgArgThrAsnGluProGlnLysLeuLysValLeuLeuArgAs 228
Db 767 AGCCACCATGATACACCGGACATGCGCGGATCAGGCTTCATCATCTGTGTTCTCA-- 824
QY 228 nLeuArgGlyGluGluAspSerProSerHisIleLysArgThrSerHisGluSer 246
Db 825 ----TGGCAGCAAGAGAAGACCCCAAGTCATCTTTCATCTAATCTCAAGAACT 875

RESULT 14

US-09-134-001C-973
; Sequence 973, Application US/09134001C
; Patent No. 6380370

; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674

; SEQ ID NO 973
; LENGTH: 1254
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-973

Alignment Scores:

Pred. No.:	0.663	Length:	1254
Score:	83.00	Matches:	44
Percent Similarity:	38.97%	Conservative:	32
Best Local Similarity:	22.56%	Mismatches:	57
Query Match:	6.55%	Indels:	62
DB:	4	Gaps:	11

US-09-705-500A-3 (1-247) x US-09-134-001C-973 (1-1254)

QY 57 PheAlaCysLeuGluAsnSerThrCysAspThrAsp-----GlyMetTyr 71
Db 796 TTTATTAAATTGAAGAGCTACATTCGAATGATCATCATCTAAACAGGACTTAT 855
QY 72 AspIleCysLysSerPheLeuTyrSerAlaAlaLysPheAspThrGlnGlyLysAlaPhe 91

Db 856 GATGTATTCAATCTTT-----AAAGATAAGTAAAGAACTGAAGGGAAATCATTT 906
QY 92 ValLysGluSerLeuLysCysIleAlaAsnGlyValThrSerLysValPheLeuAlaIle 111
Db 907 TATAGATTGAACGTACGC-----ATTATAGTGAAGACATTATTGCACCA 951
QY 112 ArgArgCysSerThrPheGlnArgMetIleAlaGluValGlnGluCysTyrSerLys 131
Db 952 CAAGATTTTAATTCATTAATAAAGAAATGATTACTGAGTTTGAAGAAAC-----999
QY 132 LeuAsnValCysSerIleAlaLysArgAsnProGluAlaIleThrGluValValGlnLeu 151
Db 999 -----999
QY 152 ProAsnHisPheSerAsnArgTyrTyrAsnArgLeuValArgSerLeuLeuGluCysAsp 171
Db 1000 GAAATCAATTTGTT-----TTTATTCGAAGATTAAATCTTCAATATGTTCAAAATGAC 1053
QY 172 GluAspThrValSerThrIleArgAspSerLeuMetGluLysIleGlyProAsnMet--- 190
Db 1054 GAAATGCCAATA-----GTTAAAGAGTTTTTCACCAGATTACTT 1092
QY 191 -----AlaSerLeuPheHisIleLeuGlnThrAspHisCysAlaGlnThrHisProArg 208
Db 1093 GATGATGCGTCACCTTTTGTATTCGGCAATGACTGAT-----TTATATCTTAAATCCAAGG 1146
QY 209 Ala-----AspPheAsnArg-----ArgArgThrAsnGluPro 219
Db 1147 GCTTCTAAGTTTTTAGATGACTATAATGTAATGTAAGTTGAGTTAGTCAATCATGCA 1206
QY 220 GlnLysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAsp 234
Db 1207 GAAAGACTT-----TTAAAGCATGAATGAGAGTGAAACAAAT 1245

RESULT 15

US-09-134-001C-1833
; Sequence 1833, Application US/09134001C
; Patent No. 6380370

; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674

; SEQ ID NO 1833
; LENGTH: 1089
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-1833

Alignment Scores:

Pred. No.:	0.715	Length:	1089
Score:	82.00	Matches:	54
Percent Similarity:	36.96%	Conservative:	48
Best Local Similarity:	19.57%	Mismatches:	106
Query Match:	6.47%	Indels:	68
DB:	4	Gaps:	13

US-09-705-500A-3 (1-247) x US-09-134-001C-1833 (1-1089)

QY 5 SerAlaValLeuLeuValLeu---ValIleSerAlaSerAlaThr-----18
Db 94 AGTCATTAACATGGCACTCTATTATTAAACAGTAACGTAACGTATGTCGGATGAA 153
QY 19 HisGluAlaGluGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsn 38

Db 154 AATCTGCAACCAAAATCAAGAAACATCACCACAAATTTTCACAGACACACCTCAAAAT 213
QY 39 SerAlaGluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAla 58
Db 214 AATCTGNA-----AATACAGATGCCACAGCCATAACA 246
QY 59 CysLeuGluAsnSerThrCysAspThr-----AspGlyMetTyrAspIleCysLysSer 76
Db 247 ACAGATCAAAATAATAATGATGAAGAAATACGATGCGTCATATCAACTT-----CCA 300
QY 77 PheLeuTyrSerAlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeu 96
Db 301 ATTCTTTATGTAACCTGCTGGCTAGATGATCAAGGAAAT---ATTATTAAAGATGCTGTG 357
QY 97 Lys----- 97
Db 358 GAAGATGTAAACCCCTCTTCAGNAAGGCAACCGGTGAAATTCCTGGGTACCAACAT 417
QY 98 -----CysIleAlaAsnGlyValThrSerLysValPheLeuAlaIleArgCys 114
Db 418 TATAGAACCTTCTGTGAGTCAGCGAATTACTAAGTTTATTAT-----CGTAAATTT 468
QY 115 SerThrPheGlnArgMetIleAlaGluValGlnGluCysTyrSerLysLeuAsnVal 134
Db 469 AGCACTGCACAATACCTATGCTTGAATAATAATCAACAAGATATAATAACAATAAAGTT 528
QY 135 CysSerIleAlaLysArgAsnProGluAlaIleThrGluValValGlnLeuProAsnHis 154
Db 529 GTTGAACACCAACCAATAAATAAGATGAAGTGAATGGNAAGAACA-----AATCAA 582
QY 155 PheSerAsnArgTyrTyrAsnArgLeuValArgSerLeuLeuGluCysAspGluAspThr 174
Db 583 GCAATATCTTCAGTAACAAATACACAAATT---ACCAAAACGAGAGAAAGACGACACACA 639
QY 175 ValSerThrIleArgAspSerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPhe 194
Db 640 ---AAAACACTAAAGAAAGATAAAGATGAGAAAGAAATCTTAAAGACACACAAAAACA----- 690
QY 195 HisIleLeuGlnThrAspHisCysAlaGlnThrHisProAlaAspPheAsnArgArg 214
Db 691 -----CCAAAGAAAGACAAAGAAAGAAA 714
QY 215 ArgThrAsnGluPro-----GlnLysLeuLysValLeuLeuArgAsnLeu 229
Db 715 GACATAAAAACTCCGAAGAAAGATAGAGAGAGAAAAAACCCAGTAATACCAAGTAACGGT 774
QY 230 ArgGlyGluGluAspSerProSerHisIleLysArgThrSerHisGlu 245
Db 775 AAAGTCGAGAAAGACGACACACAAAAACACCAAAAAAAGACAAAGAA 822

Search completed: June 12, 2003, 21:15:31
Job time : 84 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 12, 2003, 20:50:19 ; Search time 142 Seconds
(without alignments)
2434.407 Million cell updates/sec

Title: US-09-705-500A-3

Perfect score: 1268

Sequence: 1 MLQNSALLVLIVISATHE.....NLRGEDSPSHKRTSHESA 247

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 870385 seqs, 699768693 residues

Total number of hits satisfying chosen parameters: 1740770

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+p2n.model -DEV=xlp
-Q=/cgn2_1/USPTO.spool/US09705500/runat_06062003_113614_7552/app.query.fasta_1.391
-DB=Published Applications NA -QFM=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPECL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=diobsum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US09705500 @cgn 1 1 104 @runat_06062003_113614_7552
-NCPU=6 -ICPU=3 -NO WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DRV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA:*

1: /cgn2_6/ptodata/2/pubna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/2/pubna/PCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/2/pubna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/2/pubna/US07_NEW_PUB.seq.*
5: /cgn2_6/ptodata/2/pubna/PCTUS_PUBCOMB.seq.*
6: /cgn2_6/ptodata/2/pubna/US08_NEW_PUB.seq.*
7: /cgn2_6/ptodata/2/pubna/US08_NEW_PUB.seq.*
8: /cgn2_6/ptodata/2/pubna/US08_PUBCOMB.seq.*
9: /cgn2_6/ptodata/2/pubna/US09_NEW_PUB.seq.*
10: /cgn2_6/ptodata/2/pubna/US09_PUBCOMB.seq.*
11: /cgn2_6/ptodata/2/pubna/US10_NEW_PUB.seq.*
12: /cgn2_6/ptodata/2/pubna/US10_PUBCOMB.seq.*
13: /cgn2_6/ptodata/2/pubna/US60_NEW_PUB.seq.*
14: /cgn2_6/ptodata/2/pubna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	1268	100.0	771	12	US-10-116-051-1
2	1268	100.0	1283	10	US-09-840-989A-1
3	1268	100.0	3765	12	US-10-044-090-638
4	1268	100.0	3897	9	US-10-198-846-13651

Sequence 1, Appli
Sequence 1, Appli
Sequence 638, App
Sequence 13651, A

5	1250	98.6	2572	10	US-09-925-300-486	Sequence 486, App
6	861	67.9	585	10	US-09-778-120-149	Sequence 149, App
7	861	67.9	585	10	US-09-910-689-149	Sequence 149, App
8	861	67.9	585	12	US-10-010-742-149	Sequence 149, App
9	861	67.9	585	12	US-10-010-742-149	Sequence 2677, Ap
10	508	40.1	420	10	US-09-778-320-141	Sequence 141, App
11	508	40.1	420	10	US-09-910-689-141	Sequence 141, App
12	508	40.1	420	12	US-10-010-742-141	Sequence 141, App
13	396	31.2	436	9	US-09-918-995-33032	Sequence 33032, A
14	370	29.2	219	10	US-09-864-761-21309	Sequence 21309, A
15	354	27.9	2759	9	US-10-198-846-9993	Sequence 9993, Ap
16	354	27.9	4173	9	US-10-071-766-128	Sequence 128, App
17	352	27.8	892	10	US-09-361-736-1	Sequence 1, Appli
18	214	16.9	362	10	US-09-864-761-4563	Sequence 4563, Ap
19	95	7.5	4420	9	US-09-986-234-5	Sequence 5, Appli
20	91	7.2	4348	9	US-09-828-062-5	Sequence 142, App
21	90	7.1	1384	9	US-09-983-802-142	Sequence 9703, Ap
22	86.5	6.8	1383	9	US-09-764-891-9703	Sequence 169, App
23	86	6.8	1536	10	US-09-734-569-169	Sequence 119, App
24	84.5	6.7	591	10	US-09-734-569-119	Sequence 163, App
25	84	6.6	10096	10	US-09-960-253-163	Sequence 241, App
26	83	6.5	3574	10	US-09-962-832-241	Sequence 9921, Ap
27	83	6.5	4386	9	US-10-198-846-9921	Sequence 1432, Ap
28	82.5	6.5	5204	9	US-09-938-842A-1432	Sequence 2, Appli
29	81	6.4	2160	10	US-09-419-305-2	Sequence 3, Appli
30	81	6.4	2160	10	US-09-419-305-5	Sequence 13438, A
31	81	6.4	249487	9	US-10-026-188-3	Sequence 11, Appli
32	80	6.3	1067	9	US-10-198-846-13438	Sequence 1, Appli
33	79	6.2	1690	9	US-10-115-928-27	Sequence 1, Appli
34	78	6.2	185695	9	US-10-020-141-11	Sequence 1, Appli
35	78	6.2	185695	9	US-10-017-721-1	Sequence 1, Appli
36	78	6.2	640681	10	US-09-790-988-1	Sequence 781, App
37	77.5	6.1	1392	9	US-09-938-842A-781	Sequence 54, Appli
38	77.5	6.1	1944	9	US-10-102-806-54	Sequence 473, App
39	77.5	6.1	4120	10	US-09-070-927A-473	Sequence 1376, Ap
40	77	6.1	7359	9	US-10-092-154-1376	Sequence 1377, Ap
41	77	6.1	7359	9	US-10-092-154-1377	Sequence 1376, Ap
42	77	6.1	7359	10	US-09-764-847-1376	Sequence 1377, Ap
43	77	6.1	7359	10	US-09-764-847-1377	Sequence 1377, Ap
44	76.5	6.0	2421	10	US-09-974-300-1541	Sequence 1541, Ap
45	76.5	6.0	2693	9	US-10-126-467B-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-10-116-051-1
; Sequence 1, Application US/10116051
; Patent No. US20020146791A1
; GENERAL INFORMATION:
; APPLICANT: Olsen et al.
; TITLE OF INVENTION: CORPUSCLES OF STANNIUS PROTEIN, STANNIOCALCIN
; FILE REFERENCE: P108P1D1C1
; CURRENT APPLICATION NUMBER: US/10/116.051
; CURRENT FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 09/312,610
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 08/431,117
; PRIOR FILING DATE: 1995-04-28
; PRIOR APPLICATION NUMBER: 08/208,005
; PRIOR FILING DATE: 1994-03-08
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 1
; LENGTH: 771
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-116-051-1

Alignment Scores: 4.16e-169 Length: 771
Pred. No.: 1268.00 Matches: 247
Score: 100.00%
Percent Similarity: 100.00%
Conservative: 0

Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	12	Gaps:	0
US-09-705-500A-3 (1-247) x US-10-116-051-1 (1-771)			
Qy	1	MetLeuGlnAsnSerAlaValLeuLeuValLeuValLleSerAlaSerAlaThrHisGlu	20
Db	16	ATGCTCCAAACCTCAGCAGTGCTTCTGTGTGTGTGATCAGTGCTTCTGCAACCCATGAG	75
Qy	21	AlaGluGlnAsnAspSerValSerProArgLysserArgValAlaAlaGlnAsnSerAla	40
Db	76	GCGGAGCAGAACTACTCTGTGAGCCCCAGGAAATCCCGAGTGGGGGCCAAACTCAGCT	135
Qy	41	GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu	60
Db	136	GAAGTGGTTCGTGGCTCAACAGTGCTCTACAGGTTCGGCTGCGGGGGCTTTTGCATGCTG	195
Qy	61	GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysserPheLeuTyrSer	80
Db	196	GAAACTCCACCTGTGACACATGGGATGATGACATCTGTAATCTCTTGTGTACGC	255
Qy	81	AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAla	100
Db	256	GCTGCTAAATTTGACACTCAGGGAAAGCATTCGTCAAAGAGAGCTTTAAATGCATCGCC	315
Qy	101	AsnGlyValThrSerLyssValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet	120
Db	316	AACGGGGTCACCTCCAAGGTCTTCCTCGCCATTCGGAGGTGCTCCACTTTTCCAAAGGATG	375
Qy	121	IleAlaGluValGlnGluLucystrSerLyssLeuAsnValCysSerIleAlaLysArg	140
Db	376	ATTGCTGAGTGCAGNAGAGTGTCTACAGCAAGCTGAATGTGTGCAGCATTCGCCAAGCGG	435
Qy	141	AsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyr	160
Db	436	AACCCCTGAAGCCATCAGTGAGTCTCCAGATGTCGCCAATCACTTCTCCAAACAGATCAT	495
Qy	161	AsnArgLeuValArgSerLeuLeuLucyAspGluAspThrValSerThrIleArgAsp	180
Db	496	AACAGACTTGTCCGAAGCTGCTGGAATGTATGAACACACAGTCAGCACAACTCAGAGAC	555
Qy	181	SerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp	200
Db	556	AGCCTGATGGAGAAAATTGGGCCTTAACATGCCAGCTCTTCCACATCCTTCGACAGAC	615
Qy	201	HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgArgThrAsnGluProGln	220
Db	616	CACTGTGCCCAACACACCCAGAGCTGACTTCCAAAGGAGACGCACCAATGAGCCGCGAG	675
Qy	221	LysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHisIleLys	240
Db	676	AGAGTGAAGAGTCTCTCTCAGGNACCTCCGAGGTGAGGAGGACTCTCCCTCCCACATCAA	735
Qy	241	ArgThrSerHisGluSerAla	247
Db	736	CGCACATCCCATGAGAGTGCA	756

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RESULT 2
US-09-840-989A-1
; Sequence 1, Application US/09840989A
; Patent No. US20020042372A1
; GENERAL INFORMATION:
; APPLICANT: Olsen et al.
; TITLE OF INVENTION: Stanniocalcin Polynucleotides, Polypeptides, and Methods Based Thereon
; FILE REFERENCE: PF108P2
; CURRENT APPLICATION NUMBER: US/09/840,989A
; CURRENT FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: PCT/US00/29432
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,740
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 12

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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1283
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (45)..(788)
; OTHER INFORMATION:
; NAME/KEY: misc feature
; LOCATION: (857)..(857)
; OTHER INFORMATION: n is equal to a, t, c, or g.
; NAME/KEY: misc feature
; LOCATION: (1254)..(1254)
; OTHER INFORMATION: n is equal to a, t, c, or g.
; NAME/KEY: misc feature
; LOCATION: (1279)..(1279)
; OTHER INFORMATION: n is equal to a, t, c, or g.
; US-09-840-989A-1

Alignment Scores:
Pred. No.: 9.79e-169
Score: 1268.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 10
Length: 1283
Matches: 247
Conservative: 0
Mismatches: 0
Indels: 0
Gaps: 0

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US-09-705-500A-3 (1-247) x US-09-840-989A-1 (1-1283)

Qy	1	MetLeuGlnAsnSerAlaValLeuLeuValLeuValIleSerAlaSerAlaThrHisGlu	20
Db	45	ATGCTCCAAAACCTCAGCAGTGCTTCTGGTGCTGGTGATCAGTGCTTCTGCAACCCATGAG	104
Qy	21	AlaGluGlnAsnAspSerValSerProArgIlySerArgValAlaAlaGlnAsnSerAla	40
Db	105	GCGGAGCAGAAATGACTCTGTGAGCCCCAGGAAATCCCGAGTGGCGGCCCAAAACATCAGCT	164
Qy	41	GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu	60
Db	165	GAAGTGCTTGGTTGCCTCAACAGTGCTCTACAGGTGGCTGCGGGGCTTTTGCATGCCGTG	224
Qy	61	GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer	80
Db	225	GAAACATCCACCTGTGACACAGATGGGATGTATGACATCTGTAAATCCTTCTGTGACAGC	284
Qy	81	AlaAlaIlysPheAspThrGlnGlyLysAlaPheValIlysGluSerLeuLysCysIleAla	100
Db	285	GCTGCTAAATTTGACATCAGGGAAAGCATTGCTCAAGAGAGAGCTTAAATGTCATCGCC	344
Qy	101	AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet	120
Db	345	AACGGGGTCACTCCAAAGTCTTCTCGCCATTGGAGGTGCTCCACITTCCTCAAGGATG	404
Qy	121	IleAlaGluValGlnGluCysTyrSerIlysLeuAsnValCysSerIleAlaIlysArg	140
Db	405	ATTGCTCAGGTGCGAGGAAGAGTGTGTACAGAAAGTGAATGTGTGAGCATGCCAAGCGG	464
Qy	141	AsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyr	160
Db	465	AAACCTGAAGCCATCACTGAGGTGCTCCAGTGTGCCCAATCACTTCTCCAACAGATACTAT	524
Qy	161	AsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp	180
Db	525	AACAGACTTGTCCGAAGCCCTGCTGGAAATGTGATGAAGACACAGTCAGACAATCATAGAGAC	584
Qy	181	SerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp	200
Db	585	AGCCTGATGAGAAAAATTTGGCCCTAAACATGGCCACGCTCTTCCACATCCTGACACAGAC	644
Qy	201	HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgArgThrAsnGluProGln	220
Db	645	CACGTGCCCAAAACACACCCACGAGCTGACTTCAACAGGAGACGCACCAATGAGCGCGAG	704

; CURRENT FILING DATE: 2001-02-06
; NUMBER OF SEQ ID NOS: 301
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 149
; LENGTH: 585
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(585)
; OTHER INFORMATION: n=A,T,C or G
US-09-778-320-149

Alignment Scores:
Pred. No.: 8.3e-112 Length: 585
Score: 861.00 Matches: 166
Percent Similarity: 98.22% Conservative: 0
Best Local Similarity: 98.22% Mismatches: 3
Query Match: 67.90% Indels: 0
DB: 10 Gaps: 0

US-09-705-500A-3 (1-247) x US-09-778-320-149 (1-585)

QY 79 TyrSerAlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCys 98
DB 6 TACANCACTGCTAAATTTGACACTNANGGAAAGCAATTCGTCAAAGAGAGCTTAAATGTC 65
QY 99 IleAlaAsnGlyValThrSerLysValPheLeuAlaIleAtgArgCysSerThrPheGln 118
DB 66 ATCGCAACGGGGTCACCTCCAAAGGCTCTTCGCGCAATTCGGAGGTCTCCACTTTCCAA 125
QY 119 ArgMetIleAlaGluValGlnGluCysTyrSerLysLeuAsnValCysSerIleAla 138
DB 126 AGGATGATTGCTGAGGTGCGAGGAGAGTGCTACACCAAGCTGAATGTGTGAGCATCGCC 185
QY 139 LysArgAsnProGluAlaIleThrGluValGlnLeuProAsnHisPheSerAsnArg 158
DB 186 AAGCGGAACCCCTGAAGCCATCACTGAGGTCTGCCAGCTGCCCAATCACTTCTCCAAACA 245
QY 159 TyrTyrAsnArgLeuValArgSerLeuLysGluCysAspGluAspThrValSerThrIle 178
DB 246 TACTATAACAGACTTGTCCGAAGCTGCTGGAATGTGATGAAGACACACATCTCCACATCTGCAG 305
QY 179 ArgAspSerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGln 198
DB 306 AGAGACAGCTGATGGAGAAATTTGGCTTAACATGGCCAGCTCTTCCACATCTGCAG 365
QY 199 ThrAspHisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgThrAsnGlu 218
DB 366 ACAGACCACTGTGCCCAACACACCCACGAGCTGACTTCAACAGGAGACGCACCAATGAG 425
QY 219 ProGlnLysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHis 238
DB 426 CGCAGAGAGCTGAAAGTCTCTCTCAGGAACCTCCGAGGTGAGGAGACTCTCCCTCCCAAC 485
QY 239 IleLysArgThrSerHisGluSerAla 247
DB 486 ATCAACGACACATCCCATGAGAGTGCA 512

RESULT 7

US-09-910-689-149
; Sequence 149, Application US/09910689
; Patent No. US20020081609A1
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Day, Craig H.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Wang, Tonglong
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.491C6
; CURRENT APPLICATION NUMBER: US/09/910.689
; CURRENT FILING DATE: 2001-07-20
; NUMBER OF SEQ ID NOS: 307
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 149
; LENGTH: 585
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 10, 30, 32, 527, 565
; OTHER INFORMATION: n = A,T,C or G
US-09-910-689-149

Alignment Scores:
Pred. No.: 8.3e-112 Length: 585
Score: 861.00 Matches: 166
Percent Similarity: 98.22% Conservative: 0
Best Local Similarity: 98.22% Mismatches: 3
Query Match: 67.90% Indels: 0
DB: 10 Gaps: 0

US-09-705-500A-3 (1-247) x US-09-910-689-149 (1-585)

QY 79 TyrSerAlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCys 98
DB 6 TACANCACTGCTAAATTTGACACTNANGGAAAGCAATTCGTCAAAGAGAGCTTAAATGTC 65
QY 99 IleAlaAsnGlyValThrSerLysValPheLeuAlaIleArgCysSerThrPheGln 118
DB 66 ATCGCAACGGGGTCACCTCCAAAGGCTCTTCGCGCAATTCGGAGGTCTCCACTTTCCAA 125
QY 119 ArgMetIleAlaGluValGlnGluCysTyrSerLysLeuAsnValCysSerIleAla 138
DB 126 AGGATGATTGCTGAGGTGCGAGGAGAGTGCTACACCAAGCTGAATGTGTGAGCATCGCC 185
QY 139 LysArgAsnProGluAlaIleThrGluValGlnLeuProAsnHisPheSerAsnArg 158
DB 186 AAGCGGAACCCCTGAAGCCATCACTGAGGTCTGCCAGCTGCCCAATCACTTCTCCAAACA 245
QY 159 TyrTyrAsnArgLeuValArgSerLeuLysGluCysAspGluAspThrValSerThrIle 178
DB 246 TACTATAACAGACTTGTCCGAAGCTGCTGGAATGTGATGAAGACACACATCTCCACATCTGCAG 305
QY 179 ArgAspSerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGln 198
DB 306 AGAGACAGCTGATGGAGAAATTTGGCTTAACATGGCCAGCTCTTCCACATCTGCAG 365
QY 199 ThrAspHisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgThrAsnGlu 218
DB 366 ACAGACCACTGTGCCCAACACACCCACGAGCTGACTTCAACAGGAGACGCACCAATGAG 425
QY 219 ProGlnLysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHis 238
DB 426 CGCAGAGAGCTGAAAGTCTCTCTCAGGAACCTCCGAGGTGAGGAGACTCTCCCTCCCAAC 485
QY 239 IleLysArgThrSerHisGluSerAla 247
DB 486 ATCAACGACACATCCCATGAGAGTGCA 512

RESULT 8

US-10-010-742-149
; Sequence 149, Application US/10010742
; Patent No. US20020146727A1
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Day, Craig H.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Wang, Tonglong

; APPLICANT: McNeill, Patricia D.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Bennington, Angela Ann
; APPLICANT: Zehentner, Barbara
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.491C7
; CURRENT APPLICATION NUMBER: US/10/010,742
; CURRENT FILING DATE: 2001-11-30
; NUMBER OF SEQ ID NOS: 307
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 149
; LENGTH: 585
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; LOCATION: 10, 30, 32, 527, 565
; OTHER INFORMATION: n = A, T, C or G
US-10-010-742-149

Alignment Scores:
Pred. No.: 8.3e-112 Length: 585
Score: 861.00 Matches: 166
Percent Similarity: 98.22% Conservative: 0
Best Local Similarity: 98.22% Mismatches: 3
Query Match: 67.90% Indels: 0
DB: 12 Gaps: 0

US-09-705-500A-3 (1-247) x US-10-010-742-149 (1-585)

QY 79 TyrSerAlaAlaLysPheAspThrGlnGlyLysAlaPheValLysSerLeuLysCys 98
|||
DB 6 TACANCACTGCTAAATTTGACACTNAGGAAAGCATTCGTCAAGAGAGCTTAAATATGC 65
|||
QY 99 IleAlaAsnGlyValThrSerLysValPheLeuAlaLleArgArgCysSerThrPheGln 118
|||
DB 66 ATCGCCNACGGGGTCACCTCCAGGTCTTCCTCGCATTCGGAGGTCTCCACTTTCCAA 125
|||
QY 119 ArgMetIleAlaGluValGlnGluCysTyrSerLysLeuAsnValCysSerIleAla 138
|||
DB 126 AGGATGATTCGTGAGTGCAGGAAGTCTACAGCAAGCTGAATGTGTGCAGCATCGCC 185
|||
QY 139 LysArgAsnProGluAlaLleThrGluValValGlnLeuProAsnHisPheSerAsnArg 158
|||
DB 186 AAGCGGAACCCCTGAAGCCCATCACTAGGTCGTCCAGCTGCCCAATCACTTCTCCAAACAGA 245
|||
QY 159 TyrTyrAsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIle 178
|||
DB 246 TACTATACAGACTTGTCCGAGCTCTGGAAATGTGATGAGACACAGTACGACATC 305
|||
QY 179 ArgAspSerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGln 198
|||
DB 306 AGAGACAGCTCATGGAGAAATTTGGCCCTAACATGGCCAGCTCTTCCACATCTGCGAG 365
|||
QY 199 ThrAspHisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgThrAsnGlu 218
|||
DB 366 ACAGACCACTGTGCCCAACACACCCAGCTGATTCACAGGAGCGCACCAATGAG 425
|||
QY 219 ProGlnLysLysValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHis 238
|||
DB 426 CGCGAGAGCTGAAGTCTCTCTCAGGAACCTCCGAGGTGAGGAGACTCTCCCTCCAC 485
|||
QY 239 IleLysArgThrSerHisGluSerAla 247
|||
DB 486 ATCAAACGCACATCCCATGAGAGTGCA 512
|||

RESULT 9

US-10-060-036-2677/c
; Sequence 2677, Application US/10060036
; Publication No. US20030073144A1

; GENERAL INFORMATION:
; APPLICANT: Benson, Darin R.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Persing, David H.
; APPLICANT: Hepler, William T.
; APPLICANT: Jiang, Yugu
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.566
; CURRENT APPLICATION NUMBER: US/10/060,036
; CURRENT FILING DATE: 2002-01-30
; NUMBER OF SEQ ID NOS: 4560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2677
; LENGTH: 473
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-036-2677

Alignment Scores:
Pred. No.: 1.16e-87 Length: 473
Score: 689.00 Matches: 132
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 54.34% Indels: 0
DB: 9 Gaps: 0

US-09-705-500A-3 (1-247) x US-10-060-036-2677 (1-473)

QY 116 ThrPheGlnArgMetIleAlaGluValGlnGluCysTyrSerLysLeuAsnValCys 135
|||
DB 472 ACTTTCACCAAGGATGATTGCTGAGTGCAGGAAGTGTCTACGCAAGCTCAATGTGTGC 413
|||
QY 136 SerIleAlaLysArgAsnProGluAlaLleThrGluValValGlnLeuProAsnHisPhe 155
|||
DB 412 AGCATGCCCAAGCGGAACCCCTGAAGCCCATCACTGAGGTCTGCCAGCTGCCCAATCATT 353
|||
QY 156 SerAsnArgTyrTyrAsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrVal 175
|||
DB 352 TCCACAGATACTATATACAGACTTGTCCGAAGCTCTGGAAATGTGATGAGACACATGC 293
|||
QY 176 SerThrIleArgAspSerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHis 195
|||
DB 292 AGCAATACAGACAGACGCTGATGGAGAAATTTGGCTTAACATGGCCAGCTCTTCCAC 233
|||
QY 196 IleLeuGlnThrAspHisCysAlaGlnThrHisProArgAlaAspPheAsnArgArg 215
|||
DB 232 ATCTGTGAGACAGACACCACTGTGCCCAACACACCCAGCTGATCTTCAACAGGAGAGC 173
|||
QY 216 ThrAsnGluProGlnLysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSer 235
|||
DB 172 ACCAATGAGCCGCAAGAGCTGAAAGTCTCTCTCAGGAACCTCCGAGGTGAGGAGACTCT 113
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QY 236 ProSerHisIleLysArgThrSerHisGluSerAla 247
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DB 112 CCCTCCCAATCAACAGCACATCCCATGAGAGTGCA 77
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RESULT 10

US-09-778-320-141
; Sequence 141, Application US/09778320
; Patent No. US20010034052A1
; GENERAL INFORMATION:

; APPLICANT: Dillon, Davin C.
; APPLICANT: Day, Craig H.
; APPLICANT: Jiang, Yugu
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Wang, TongTong
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.491C5

; CURRENT APPLICATION NUMBER: US/09/778,320
; CURRENT FILING DATE: 2001-02-06
; NUMBER OF SEQ ID NOS: 301
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 141
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 20, 21, 23, 28, 155, 174, 221, 239, 240, 258, 265, 302, 307,
; LOCATION: 316, 342, 346, 374, 387, 388, 402, 418
; OTHER INFORMATION: n = A,T,C or G
US-09-778-320-141

Alignment Scores:
Pred. No.: 3,546-62 Length: 420
Score: 508.00 Matches: 116
Percent Similarity: 82.27% Conservativity: 0
Best Local Similarity: 82.27% Mismatches: 19
Query Match: 40.06% Indels: 6
DB: 10 Gaps: 0

US-09-778-320-141 x US-09-778-320-141 (1-420)

QY 85 AspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAlaAsnGlyValThr 104
Db 1 GACACTCAGGGAAGCATNNGCNAANAGAGCTTAAATGCGATGCCCAACGGGGTCACC 60
QY 105 SerLysValPheLeuAlaIleArgCysSerThrPheGlnArgMetIleAlaGluVal 124
Db 61 TCCAGAGTCTTCTCGCCATTGGAGGTGCTCCACTTTCAAAGGATGATTGCTGAGGTG 120
QY 125 GlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArgAsnProGluAla 144
Db 121 CAGGAAGAGTGTACAGCAAGCTGAATGTGGCANCATGCCAAGCGGAACCCNGAGCC 180
QY 145 IleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyrAsnArgLeuVal 164
Db 181 ATCACTGAGTGTGTCAGCTGCCAATCACTTCTCCACANATCTATAACAGACTTGN 240
QY 165 ArgSerLeuGluCysAspGluAspThr-ValSerThrIleArg-AspSerLeuMetG 184
Db 241 CGAAGCTGTGGAATGNGATGAANACACAGGCGAGCAACAATCAGGAGACACCTGATGG 300
QY 184 LuLysIleGlyProAsnMetAla-SerLeuPheHisIleLeu--GlnThrAspHisCysA 203
Db 301 ANAAANTGGGCTTANCATGGCCAGGCTCTTCCACATCTCTGNCANGACAGACCTGTG 360

RESULT 11

US-09-910-689-141
; Sequence 141, Application US/09910689
; Patent No. US20020081609A1
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Wang, Tongtong
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.491C6
; CURRENT APPLICATION NUMBER: US/09/910,689
; CURRENT FILING DATE: 2001-07-20
; NUMBER OF SEQ ID NOS: 307
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 141

; LENGTH: 420

; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 20, 21, 23, 28, 155, 174, 221, 239, 240, 258, 265, 302, 307,
; LOCATION: 316, 342, 346, 374, 387, 388, 402, 418
; OTHER INFORMATION: n = A,T,C or G
US-09-910-689-141

Alignment Scores:
Pred. No.: 3,546-62 Length: 420
Score: 508.00 Matches: 116
Percent Similarity: 82.27% Conservativity: 0
Best Local Similarity: 82.27% Mismatches: 19
Query Match: 40.06% Indels: 6
DB: 10 Gaps: 0

US-09-705-500A-3 (1-247) x US-09-910-689-141 (1-420)

QY 85 AspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAlaAsnGlyValThr 104
Db 1 GACACTCAGGGAAGCATNNGCNAANAGAGCTTAAATGCGATGCCCAACGGGGTCACC 60
QY 105 SerLysValPheLeuAlaIleArgCysSerThrPheGlnArgMetIleAlaGluVal 124
Db 61 TCCAGAGTCTTCTCGCCATTGGAGGTGCTCCACTTTCAAAGGATGATTGCTGAGGTG 120
QY 125 GlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArgAsnProGluAla 144
Db 121 CAGGAAGAGTGTACAGCAAGCTGAATGTGGCANCATGCCAAGCGGAACCCNGAGCC 180
QY 145 IleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyrAsnArgLeuVal 164
Db 181 ATCACTGAGTGTGTCAGCTGCCAATCACTTCTCCACANATCTATAACAGACTTGN 240
QY 165 ArgSerLeuGluCysAspGluAspThr-ValSerThrIleArg-AspSerLeuMetG 184
Db 241 CGAAGCTGTGGAATGNGATGAANACACAGGCGAGCAACAATCAGGAGACACCTGATGG 300
QY 184 LuLysIleGlyProAsnMetAla-SerLeuPheHisIleLeu--GlnThrAspHisCysA 203
Db 301 ANAAANTGGGCTTANCATGGCCAGGCTCTTCCACATCTCTGNCANGACAGACCTGTG 360
QY 203 laGlnThrHisProArg-AlaAspPheAsnArgArgThrAsnGluPro 219
Db 361 CCCAAACACACCCNCTGAGCTGACTTNNACAGGAGACGCACNAGAGGCC 411

RESULT 12

US-10-010-742-141
; Sequence 141, Application US/10010742
; Patent No. US20020146727A1
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Day, Craig H.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Wang, Tongtong
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Bennington, Angela Ann
; APPLICANT: Zehentner, Barbara
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.491C7
; CURRENT APPLICATION NUMBER: US/10/010,742
; CURRENT FILING DATE: 2001-11-30
; NUMBER OF SEQ ID NOS: 307
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 141

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; LENGTH: 420
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 20, 21, 23, 28, 155, 174, 221, 239, 240, 258, 265, 302, 307,
; LOCATION: 316, 342, 346, 374, 387, 388, 402, 418
; OTHER INFORMATION: n = A,T,C or G
US-10-010-742-141

Alignment Scores:
Pred. No.: 3,54e-62 Length: 420
Score: 508.00 Matches: 116
Percent Similarity: 82.27% Conservatives: 0
Best Local Similarity: 82.27% Mismatches: 19
Query Match: 40.06% Indels: 6
DB: 12 Gaps: 0

US-09-705-500A-3 (1-247) x US-10-010-742-141 (1-420)

QY 85 AspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAlaAsnGlyValThr 104
DB 1 GACACTCAGGGAAGACATNGNCAANAGAGCTTAAATGTCATGCCAACGGGTGACC 60

QY 105 SerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMetIleAlaGluVal 124
DB 61 TCCAAGTCTTCTCGCCATTGGAGTGTCTCCACTTTCCAAAGGATGATTCTGAGGTG 120

QY 125 GlnGluGlyCysTyrSerLysLeuValCysSerIleAlaLysArgAsnProGluAla 144
DB 121 CAGGAAGAGTGTACAGCAAGCTGATGTGCGCANCATGCCAAGCGGAACCCNGAAGCC 180

QY 145 IleThrGluValValGlnLeuProHisPheSerAsnArgTyrTyrAsnArgLeuVal 164
DB 181 ATCATGAGTGTGTCAGCTGCGCATCACTTCTCCAAACATTAATTAACAGATTGNN 240

QY 165 ArgSerLeuLeuGluCysAspGluAspThr-ValSerThrIleArg-AspSerLeuMetG 184
DB 241 CGAAGCTCTCGAATGNGATGAANACACAGGCGCAGCACAAATCAGGAGACGCTGATGG 300

QY 184 LuLysIleGlyProHisMetAla-SerLeuPheHisIleLeu--GlnThrAspHisCysA 203
DB 301 ANAAANTGGGCTTANCATGGCCAGGCTCTTCCACATCTCTGANGACAGACCACTGTG 360

QY 203 laGlnThrHisProArg-AlaAspPheAsnArgArgThrAsnGluPro 219
DB 361 CCNAAACACCCNCTGAGCTGACTTNNACAGGACGACACNAGAGGCC 411

RESULT 13
US-09-918-995-33032
; Sequence 33032, Application US/0918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT FILING DATE: 2001-07-30
; PRIOR FILING DATE: 2001-07-30
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 33032
; LENGTH: 436
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-995-33032

Alignment Scores:
Pred. No.: 2,51e-46 Length: 436
Score: 396.00 Matches: 76
Percent Similarity: 100.00% Conservatives: 0
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 31.23% Indels: 0
DB: 9 Gaps: 0

US-09-705-500A-3 (1-247) x US-09-918-995-33032 (1-436)

QY 172 GluAspThrValSerThrIleArgAspSerLeuMetGluLysIleGlyProAsnMetAla 191
DB 2 GAAGACACAGTCAGCACAAATCAGAGACAGCCTGATGGAGAAAATTGGCGCTTAACATGCC 61

QY 192 SerLeuPheHisIleLeuGlnThrAspHisCysAlaGlnThrHisProArgAlaAspPhe 211
DB 62 AGCCTCTTCCATCTCTGCAGACAGACCACTGTGCCAAAACACACCCACGAGCTCACTTC 121

QY 212 AsnArgArgThrAsnGluProGlnLysLeuLysValLeuLeuArgAsnLeuArgGly 231
DB 122 AACAGGAGACGACCAATGAGCCGCGAAGCTGAAAGTCTCTCTCAGGAACCTCCGAGGT 181

QY 232 GluGluAspSerProSerHisIleLysArgThrSerHisGluSerAla 247
DB 192 GAGGAGGAGCTCTCCCTCCACATCAAAACGCACATCCCATGAGAGTGCA 229

RESULT 14
US-09-864-761-21309/c
; Sequence 21309, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aemica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/006666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006657
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006659
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006655
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006653
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006652
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

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(without alignments)
2821.076 Million cell updates/sec

Title: US-09-705-500A-3

Perfect score: 1268

Sequence: 1 MLQNSAVLLVLVISATHE.....NLRGEDSPSHIKTSHESA 247

Scoring table:

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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6: em_estpl.*
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14: gb_est5.*
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16: em_estom.*
17: gb_gss.*
18: em_gss_hum.*
19: em_gss_inv.*
20: em_gss_pln.*
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22: em_gss_fun.*
23: em_gss_nam.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
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4	1076	84.9	648	13	BM311682	BM311682 IG60F04.x
5	1075	84.8	644	10	AW965863	AW965863 EST377936
6	1066	84.1	617	13	BM311087	BM311087 IG60F04.y
7	1041	82.1	915	13	B1182587	B1182587 UNL-P-PN-
8	1038	81.9	915	14	BQ894224	BQ894224 AGENCOURT
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21	627	49.4	930	12	BF303368	BF303368 602030289
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26	543	42.8	605	13	BI010412	BI010412 MR2-EN009
27	515	40.6	388	10	BE491299	BE491299 BP210022A
28	514	40.5	531	10	AW466127	AW466127 DB71B12.Y
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35	454	35.8	524	14	BM708153	BM708153 UI-E-C11-
36	443	34.9	492	10	BE235128	BE235128 142476 MA
37	434	34.2	543	9	AL702795	AL702795 DKF26686H
38	415	32.7	251	13	BI975654	BI975654 484119 MA
39	396	31.2	375	14	BM720350	BM720350 UI-E-EU0-
40	378.5	29.9	461	10	AW463836	AW463836 BP230013B
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43	354.5	28.0	990	11	AK002527	AK002527 Mus muscu
44	354.5	28.0	1607	11	AK010318	AK010318 Mus muscu
45	354	27.9	933	14	BQ928761	BQ928761 AGENCOURT

ALIGNMENTS

RESULT 1
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LOCUS
DEFINITION AGENCOURT 8032625 NIH_MGC_102 Homo sapiens CDNA clone IMAGE:6213518
5', mRNA sequence.
ACCESSION BQ672018
VERSION BQ672018.1 GI:21782852
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 869)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)


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Db      364 TATAACAGACTTGTCCGAGCCTGTGGAATGTGATGAGACACAGTCAGCACAAATCAGA 423
Qy      180 AspSerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThr 199
Db      424 GACAGCTGATGGAGAAATGGGCTTAATGCGCAGCCTTCCACATCTCGAGACA 483
Qy      200 AspHisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgArgThrAsnGluPro 219
Db      484 GACCACTGTGCCCAACACACACCACGAGCTGACTTCAACAGGAGACGCCACCAATGAGCG 543
Qy      220 GlnLysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHisIle 239
Db      544 CAGAAGCTGAAGTCTCTCTCAGGAACCTCCGAGGTGAGGAGACTCTCCCTCCACATC 603
Qy      240 LysArgThrSerHisGluSerAla 247
Db      604 AAACGCACATCCCATGAGAGTGCA 627

RESULT 4
LOCUS   BM311682
DEFINITION   ig60f04.x1 HR85 islet Homo sapiens cDNA 3' similar to SW:STGL_HUMAN
ACCESSION   BM311682
VERSION     BM311682.1 GI:18046027
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
REFERENCE   1 (bases 1 to 648)
AUTHORS     Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
            Lemishka,I., Scarce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
            Hillier,L., Maria,M., Pape,D., Wyllie,F., Martin,J., Blistein,A.,
            Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas
            ,M., Gibbons,M., McCann,R., Cole,R., Tsagarisvilli,R., Williams,T.,
            Jackson,Y. and Bowers,Y.
            Endocrine Pancreas Consortium
            Unpublished (2000)
            Other_ESTs: ig60f04.y1
            Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
            Endocrine Pancreas Consortium
            Harvard University, Howard Hughes Medical Institute
            Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
            MA 02138
            Tel: 617-495-1812
            Fax: 617-495-8557
            Email: dmelton@biohp.harvard.edu
            Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
            Washington University Genome Sequencing Center For information on
            obtaining a clone please contact: Dr. Hiroshi Inoue
            (hinoue@im.wustl.edu)
            Possible reversed clone: similarity on wrong strand
            Seq primer: -40UP from Gibco
            High quality sequence stop: 475.
            Location/Qualifiers
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                /db_xref="taxon:9606"
                /clone_lib="HR85 islet"
                /tissue_type="Purified pancreatic islet"
                /lab_host="DH10B"
                /note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
            NotI; Site_2: XhoI; cDNA made by oligo-dT priming.
            Size selected on agarose gel. Average insert size ~1kb. 5'
            XhoI site was destroyed after directional cloning.
            Amplified once. Contact information: Hiroshi Inoue, MD,
            Metabolism Div. (Alan Permutt Lab), Washington University
            School of Medicine, Box 8127, 660 South Euclid Ave., St.
            Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
            314-362-1916, Fax: 314-747-2692."
            175 a 179 c 164 g 130 t

BASE COUNT
ORIGIN

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Alignment Scores:
Pred. No.: 6,47e-122 Length: 648
Score: 1076.00 Matches: 207
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 84.86% Indels: 0
DB: 13 Gaps: 0

US-09-705-500A-3 (1-247) x BM311682 (1-648)
Qy      13 IleSerAlaSerAlaThrHisGluAlaGlnAsnAspSerValSerProArgLysSer 32
Db      28 ATCAGTGTCTTGTCAACCCATGAGCGGAGCAGAAATGACTCTGTGAGCCCGGAGAAATCC 87
Qy      33 ArgValAlaAlaGlnAsnSerAlaGluValValArgCysLeuAsnSerAlaLeuGlnVal 52
Db      88 CGAGTGGCGGCTCAAAATCTCAGCTGAAGTGGTTCGTTGCCTCAACAGTGCTTACAGGTC 147
Qy      53 GlyCysGlyAlaPheAlaCysLeuGluAsnSerThrCysAspThrAspGlyMetTyrAsp 72
Db      148 GCCTGGCGGGCTTTTGTGATGCTGTGAAAACCTCCACCTGTGACACAGATGGGATGTATGAC 207
Qy      73 IleCysLysSerPheLeuTyrSerAlaAlaLysPheAspThrGlnGlyLeAlaPheVal 92
Db      208 ATCTGTAATCCTTCTTGTACAGCGCTGCTAAATTTGCACACTCAGGGAAGAAAGCATTCGTC 267
Qy      93 LysGluSerLeuLysCysIleAlaAsnGlyValThrSerLysValPheLeuAlaIleArg 112
Db      268 AAAGAGAGCTTAAATGTCATCGCAACGGGGTCACTCCAAAGGTCTTCTCGCCATTCGG 327
Qy      113 ArgCysSerThrPheGlnArgMetIleAlaGluValGlnGluCysTyrSerLysLeu 132
Db      328 AGGTGCTCCACTTTCCTCAAGAGTATGCTGAGGTGCGAGGAGAGTGTCTACGACGAGCTG 387
Qy      133 AsnValCysSerIleAlaLysArgAsnProGluAlaIleThrGluValValGlnLeuPro 152
Db      388 AATGTGTGACATCGCAACGCGGAACCTCAAGCCATCATCTGAGGTGCTCGAGTGCC 447
Qy      153 AsnHisPheSerAsnArgTyrTyrAsnArgLeuValArgSerLeuGluCysAspGlu 172
Db      448 AATCACTTCTCCAACAGATACTATAACAGACTTGTCCGAAGCTGCTGGAATGTGATGAA 507
Qy      173 AspThrValSerThrIleArgAspSerLeuMetGluLysIleGlyProAsnMetAlaSer 192
Db      508 GACACAGTCAGCACATCAGACAGAGCTGTATGAGAGAAATTTGGGCTTAACATGCCACG 567
Qy      193 LeuPheHisIleLeuGlnThrAspHisCysAlaGlnThrHisProArgAlaAspPheAsn 212
Db      568 CTCCTTCCACATCTCTGACAGACAGACCACTGTGCCCAAAACACACCCAGAGCTGACTTCAAC 627
Qy      213 ArgArgThrAsnGluPro 219
Db      628 AGGAGCGCACCAATGAGCG 648

RESULT 5
LOCUS   AW965863
DEFINITION   EST377936 MAGE resequences, MAGI Homo sapiens cDNA, mRNA sequence.
ACCESSION   AW965863
VERSION     AW965863.1 GI:8155699
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
REFERENCE   1 (bases 1 to 644)
AUTHORS     Hegde,P., Qi,R., Abernathy,K., Dharap,S., Gaspar,R., Gay,C., Holt
            ,I.E., Saeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and
            Quackenbush,J.
            Assessment of gene expression patterns in a model of colon tumor
            metastasis using a 19,200 element cDNA microarray
            Unpublished (2000)
            JOURNAL

```

CONTACT: John Quackenbush
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 3528
 Fax: 301 838 0208
 Email: johnq@igr.org
 Plate: 220
 Seq primer: Reverse.

LOCUS BM311087 617 bp mRNA linear EST 03-JAN-2000
DEFINITION ig6f04.y1 HR85 islet Homo sapiens cDNA 5' similar to SW:STC1_HUMAN
 P52823 STANNOCALCIN 1 PRECURSOR ;, mRNA sequence.
ACCESSION BM311087
VERSION BM311087.1 GI:18045432
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 617)
AUTHORS Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K.,
 Lemishka, I., Scarce, M., Brestelli, J., Gradwohl, G., Clifton, S.,
 Hillier, A., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A.,
 Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas
 M., Gibbons, M., McCann, R., Cole, R., Tsagaris, V., Williams, T.,
 Jackson, Y. and Bowers, Y.
TITLE Endocrine Pancreas Consortium
JOURNAL Unpublished (2000)
COMMENT Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
 Endocrine Pancreas Consortium
 Harvard University, Howard Hughes Medical Institute
 Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
 MA 02138
 Tel: 617-495-1812
 Fax: 617-495-8557
 Email: dmelton@biohp.harvard.edu
 Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
 Washington University Genome Sequencing Center For information on
 obtaining a clone please contact: Dr. Hiroshi Inoue
 (hinoue@m.wustl.edu)
 Possible reversed clone: similarity on wrong strand
 Seq primer: -40RP from Gibco
 High quality sequence stop: 441.
FEATURES Location/Qualifiers
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 1..617
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="HR85 islet"
 /tissue_type="Purified pancreatic islet"
 /lab_host="DH10B"
 /note="Organ: Pancreas; Vector: pBluescript SK(-); Site 1:
 NotI; Site 2: XhoI; cDNA made by oligo-dT priming.
 Size-selected on agarose gel. Average insert size ~1kb. 5'
 XhoI site was destroyed after directional cloning.
 Amplified once. Contact information: Hiroshi Inoue, MD,
 Metabolism Div. (Alan Permutt Lab), Washington University
 School of Medicine, Box 8127, 660 South Euclid Ave., St.
 Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
 314-362-1916, Fax: 314-747-2692."

BASE COUNT 123 a 155 c 168 g 171 t
ORIGIN
 Alignment Scores:
 Pred. No.: 1,01e-120 Length: 617
 Score: 1066.00 Matches: 205
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 84.07% Indels: 0
 DB: 13 Gaps: 0
 US-09-705-500A-3 (1-247) x BM311087 (1-617)

QY 20 GluAlaGluInAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSer 39
 DB 617 GAGCGGAGCAGATGATGCTGTGAGCCCGAGAAATCCCGAGTGGCGGCTCAAACTCA 558
 QY 40 AlaGluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCys 59
 DB 557 GCTGAAGTGGTTCCTTCCTCAACAGTGTCTACAGTGGCTGGCGGGCTTTTGATGC 498
 QY 60 LeuGluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyr 79
 BM311087/c

Db 497 CTGGAAACTCCACCTGTGACACAGATGGATGTATGACATCTGTAATCTCTTGTGAC 438
 Qy SerAlaAlaPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIle 99
 Db 437 AGCGTGTAAATTTGACACTCAGGAAAGCATTCGTCAGAGAGAGCTTAAATGTCATC 378
 Qy 100 AlaAsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArg 119
 Db 377 GCCAACGGGGTCACTCCAGAGTCTCTCGCCATTCGGAGGTGCTCCACTTCCAAAGG 318
 Qy 120 MetIleAlaGluValGlnGluCysTyrSerLysLeuAsnValCysSerIleAlaLys 139
 Db 317 ATGATTGCTGAGGTGAGAGAGAGTCTACAGCAAGCTGAATGTGACAGATCCCAAG 258
 Qy 140 ArgAsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyr 159
 Db 257 CGGAACCTGAGCCATCACTAGGTGCTCGAGTCCAGTCCCAATCACTTCTCCACAGATAC 198
 Qy 160 TyrAsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArg 179
 Db 197 TATAACAGACTTGTCCGAAGCTGTGGAATGTGATGAAGACACAGTCAGCAATCAGA 138
 Qy 180 AspSerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThr 199
 Db 137 GACAGCTGATGAGAAATTTGGCTTAACATGGCCAGCTCTTCCACATCTCGAGACA 78
 Qy 200 AspHisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgThrAsnGluPro 219
 Db 77 GACCACTGTGCCAAACACACCCAGCTGACTTCAACAGGAGACGCCAATGAGCGG 18
 Qy 220 GlnLysLeuLysVal 224
 Db 17 CAGAAGCTGAAAGTC 3

RESULT 7

BI182587
 LOCUS
 DEFINITION UNL-P-FN-bj-f-06-0-UNL.s1 UNL-P-FN Sus scrofa cDNA clone
 UNL-P-FN-bj-f-06-0-UNL 3', mRNA sequence.

ACCESSION BI182587.1 GI:14656996

VERSION EST.

KEYWORDS pig.

SOURCE Sus scrofa

ORGANISM

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

AUTHORS 1 (bases 1 to 915)

TITLE Caetano, A.R., Johnson, R.K. and Pomp, D.

Generation and sequence characterization of a normalized cDNA

library from swine ovarian follicles

JOURNAL Unpublished (2001)

COMMENT Contact: Pomp, D

Department of Animal Science

University of Nebraska, Lincoln

Lincoln, NE 68583-0908, USA

Tel: 402 472 6416

Fax: 402 472 6362

Email: dpomp@unl.edu

Oligo-dr track not found, Not I site shown in beginning of sequence
 is likely internal to the message.

Seq primer: M13 -29

POLYA=No.

FEATURES

source

1. 915
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 /strain="University of Nebraska, Lincoln Swine Selection
 lines"

/db_xref="taxon:9823"

/clone="UNL-P-FN-bj-f-06-0-UNL"

/dev_stages="ADULT"

/lab_host="DH10B (Life Technologies)"

/note="Vector: pT73D-Pac (Pharmacia) with a modified

polylinker; Site 1: Not I; Site 2: Eco RI; The UNL-P-FN
 library is a normalized library representing porcine
 ovarian follicles, ranging between 2.0 to 10.0 mm in
 diameter, collected during 7 days of the follicular phase
 of the pig estrous cycle. This library was derived from
 the library UNL-P-F2. The tag is a string of 5-6
 nucleotides present between the Not I site and the
 oligo-dr track. The library was constructed as described
 by Bonaldo, Lennon and Soares, Genome Research 6: 791-806
 , 1996.

TAG_SEQ=None found"

BASE COUNT 221 a 249 c 216 t 10 others
 ORIGIN

Alignment Scores:

Pred. No.: 2 51e-117 Length: 915
 Score: 1041.00 Matches: 203
 Percent Similarity: 95.00% Conservative: 6
 Best Local Similarity: 92.27% Mismatches: 9
 Query Match: 82.10% Indels: 2
 DB: 13 Gaps: 0

US-09-705-500A-3 (1-247) x BI182587 (1-915)

Qy 29 ProArgLysSerArgVal-AlaAlaGlnAsnSerAlaGluValValArgCysLeuAsnSe 48

Db 24 CCANNAAAAATCCCGTTGGCAGGTGAGAACTCAAGTTGAAATGGTTGCTCCCTCAACAG 83

Qy 48 rAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeuGluAsnSerThrCysAspThrAs 68

Db 84 CGCTCTGCAGGTGGCTGTGGAGCTTTTGCTGCTGCGAAATCCACCTGTGCACAGA 143

Qy 68 pGlyMetTyrAspIleCysLysSerPheLeuTyrSerAlaAla-LysPheAspThrGln 88

Db 144 TGGGATGTACACATCTGTAATCTCTTGTACAGCGCTCTTANAATTTGACACTCAGG 203

Qy 88 lYlYsAlaPheValLysGluSerLeuLysCysIleAlaAsnGlyValThrSerLysValP 108

Db 204 GAAAGCCTTTGTCAAAGAGAGAGTTTAAAGTGCATCGCAACGGGTGTCACCGCAAGGTCT 263

Qy 108 heLeuAlaIleArgArgCysSerThrPheGlnArgMetIleAlaGluValGlnGluC 128

Db 264 TCTTCGCCATTCGGAGATGCTCTACTTTCCAGCGGATGATTCGCGAGGTGCGAGGAGT 323

Qy 128 ySTyrSerLysLeuAsnValCysSerIleAlaLysArgAsnProGluAlaIleThrGluV 148

Db 324 GCTACACCAAGCTGAAGTGTGACAGTGTGCGCAACGGGACCCCGAGCCATCAGGAG 383

Qy 148 alValGlnLeuProAsnHisPheSerAsnArgTyrTyrAsnArgLeuValArgSerLeu 168

Db 384 TCGTCCAGCTCCCAATCACTTCTCCAACAGATACTACAACAGACTTGTTCGACGCTGC 443

Qy 168 euGluCysAspGluAspThrValSerThrIleArgAspSerLeuMetGluLysIleGlyP 188

Db 444 TGGAAATGTGACGAAGACACGCTGACACCATCAGACAGCCTGATGGAGAAAAATTGGGC 503

Qy 188 roAsnMetAlaSerLeuPheHisIleLeuGlnThrAspHisCysAlaGlnThrHisPro 208

Db 504 CCAACATGGCCAGCGCTTCCACATCTTCAGACGATCACTGTGCCACAGCACCAGC 563

Qy 208 rGAlaAspPheAsnArgArgThrAsnGluProGlnLysLeuLysValLeuLeuArgA 228

Db 564 GAGCTGACTTCAACAGAAAAACGTGCCAACGAGCCACAGAGCTGAAAGTCTCTCTCAGGA 623

Qy 228 snLeuArgGlyGluGluAspSerProSerHisIleLysArgThrSerHisGluSer 246

Db 624 ACCTCCGAGGTGAGGTGGCTCTCCCGCCCAATCAACAGCACCCTCCACAGAGAGT 679

RESULT 8

BQ894224

LOCUS

DEFINITION

clone IMAGE:6180797 5', mRNA sequence.

BQ894224

LOCUS

DEFINITION

clone IMAGE:6180797 5', mRNA sequence.

BQ894224 915 bp mRNA linear EST 16-AUG-2002

AGENCOURT 8489564 lupski_dorsal_root_ganglion Homo sapiens cDNA

clone IMAGE:6180797 5', mRNA sequence.

Db 1 TCAGCAGTCTCTTGGTGTGTGATCACTGCTTCTGCACCCATCAGCGGAGCAGAAAT 60
 Qy 25 AspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAlaGluValValArg 44
 Db 61 GACTCTGTGAGCCCGAGGAATCCCGAGTGGCGGCTCAAACTCAGCTGAAGTGTTCGT 120
 Qy 45 CysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeuGluAsnSerThr 64
 Db 121 TGCCTCAACAGTCTCTACAGTCTGGTGGCGGCTTTTGATGCTGGAAATCCACC 180
 Qy 65 CysAspThrAspGlyMetTyrAspLysSerPheLeuTyrSerAlaAlaLysPhe 84
 Db 181 TGTGACACAGATGGGATGTATGATCTGTAATCTCTTGTACAGCGCTCTAAATTT 240
 Qy 85 AspThrGlnGlyAlaPheValLysGluSerLeuLysCysIleAlaAsnGlyValThr 104
 Db 241 GACACTCAGGGAAGCATCTCTCAAGAGAGCTTAAATGCTGCCAACGGGTACCC 300
 Qy 105 SerLysValPheLeuAlaIleArgCysSerThrPheGlnArgMetIleAlaGluVal 124
 Db 301 TCCAAAGTCTCTCGCCATTCGGAGTGTCTCCACTTCCAAAGGATGATTGCTGAGGTG 360
 Qy 125 GlnGluGlyCysTyrSerLysLeuAsnValCysSerIleAlaLysArgAsnProGluAla 144
 Db 361 CAGGAAGAGTGTACAGCAAGCTGAATGTGTGCAGCATGCCAACGGAACTCGAAGCC 420
 Qy 145 IleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyrAsnArgLeuVal 164
 Db 421 ATCACTGAGTCTGTCAAGTGTCCCAATCACTTCTCAACAGATATATACAGACTTGTG 480
 Qy 165 ArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAspSerLeuMetGlu 184
 Db 481 CGAAGCTGTCTGAATGTGATGAANACAGTCAGCAACAATCAGACAGCGCTGATGAG 540
 Qy 185 LysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAspHisCysAlaGln 204
 Db 541 AAAATTTGGCCCTTAC-ATTGCCAGCTCTTCCACATCTCTGCAGACAGA-CACTGTGCCCA- 597
 Qy 205 ThrHisProArgAlaAspPheAsnArgArgArgThrAsnGluProGln 220
 Db 598 ACACACCCACGAGCTGACTTTCAC-AGGAGACGCC-CAATGAGCCGCA 643

AL549427 782 bp mRNA linear EST 16-FEB-2001
 AL549427 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0D1044Y118 5
 prime, mRNA sequence.
 AL549427
 AL549427.1 GI:12885398
 EST...
 SOURCE human.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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 /clone="CS0D1044Y118"
 /clone_lib="LTI_NFL006_PL2"
 /tissue_type="placenta"
 /note="Vector: pCMVSPORT 6; Site 1: NotI; 1st strand cDNA
 was primed with a NotI-oligo(dT) primer. Five prime end
 enriched, double-stranded cDNA was digested with Not I and
 cloned into the Not I and Eco RV sites of the pCMVSPORT 6

FEATURES
 source
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 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="CS0D1044Y118"
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 was primed with a NotI-oligo(dT) primer. Five prime end
 enriched, double-stranded cDNA was digested with Not I and
 cloned into the Not I and Eco RV sites of the pCMVSPORT 6

vector. Library was normalized. Library was constructed by
 Life Technologies. Contact : Feng Liang Life Technologies,
 a division of Invitrogen 9800 Medical Center Drive
 Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
 Email : fliang@lifetech.com URL :
 http://fulllength.invitrogen.com"

BASE COUNT 230 a 204 c 202 g 144 t 2 others
 ORIGIN

Alignment Scores: 4.19e-97 Length: 782
 Score: 876.00 Matches: 177
 Percent Similarity: 98.88% Conservative: 0
 Best Local Similarity: 98.88% Mismatches: 2
 Query Match: 69.09% Indels: 1
 DB: 9 Gaps: 0

US-09-705-500A-3 (1-247) x AL549427 (1-782)

Qy 1 MetLeuGlnAsnSerAlaValLeuValLeuValIleSerAlaSerAlaThrHisGlu 20
 Db 245 ATGCTCCAAACTCAGCAGTCTTCTGGTCTGGTGATCATGCTTCTGCAACCATGAG 304
 Qy 21 AlaGluGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
 Db 305 CGCGA-SAGAATGACTCTGTGAGCCCGAGGAAATCCCGAGTGGCGGCTCAAACTCAGCT 363
 Qy 41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
 Db 364 GAACTGGTTCGTTGCCCTCAACAGTCTCTACAGTCTGGTGGCGGCTTTTGCATGCGCTG 423
 Qy 61 GluAsnSerThrCysAspThrAspGlyMetTyrAspLysSerPheLeuTyrSer 80
 Db 424 GAAACTCCACTCTGACACAGATGGATGTATGACATCTGTAATCTCTTCTGTACAGC 483
 Qy 81 AlaAlaLysPheAspThrGlnGlyAlaPheValLysGluSerLeuLysCysIleAla 100
 Db 484 GCTGCTAAATTTGACACTCAGGGGAAAGCATTCTGCAAGAGAGCTTAAATGTCATGCC 543
 Qy 101 AsnGlyValThrSerLysValPheLeuAlaIleArgCysSerThrPheGlnArgMet 120
 Db 544 AACGGGTGACCTCCAAAGGCTTCTCGCCATTCGGAGGTCTCCACTTTTCCAAAGGATG 603
 Qy 121 IleAlaGluValGlnGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
 Db 604 ATTCTGAGGTGCAGGAAGAGTGTCTACAGCAAGCTGATGTGTCAGCATGCCAAGCGG 663
 Qy 141 AsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
 Db 664 AACCTGAAAGCCATCACTGAGTGTGTCAGTGGCCCAATCACTTCTCCACAGATACTAT 723
 Qy 161 AsnArgLeuValArgSerLeuGluCysAspGluAspThrValSerThrIleArg 179
 Db 724 AACAGACTTGTCCGAAGCCTGCTGGAATGTGATGAAGACAGTYAGCAACATCAGA 780

RESULT 11
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 DEFINITION MRO-BT4501-280601-103-c11 BT4501 Homo sapiens cDNA, mRNA sequence.
 ACCESSION BQ308414
 VERSION BQ308414.1 GI:20849730
 KEYWORDS EST.
 SOURCE human.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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 /clone="MRO-BT4501-280601-103-c11 BT4501"
 /tissue_type="placenta"
 /note="Vector: pCMVSPORT 6; Site 1: NotI; 1st strand cDNA
 was primed with a NotI-oligo(dT) primer. Five prime end
 enriched, double-stranded cDNA was digested with Not I and
 cloned into the Not I and Eco RV sites of the pCMVSPORT 6

TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l1=MR0&t2=MR0-BT4501-
280601-103-clit3=2001-06-28&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 576.
Location/Qualifiers
1. .577
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="BT4501"
/dev_stage="Adult"
/note="Organ: breast; Vector: puc18; Site 1: SmaI; Site 2:
SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No. 196
716 - Ludwig Institute for Cancer Research) profiles
into the puc 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."
BASE COUNT 161 a 159 c 140 g 117 t
ORIGIN
Alignment Scores:
Pred. No.: 5,138-94 Length: 577
Score: 849.00 Matches: 183
Percent Similarity: 96.83% Conservative: 0
Best Local Similarity: 96.83% Mismatches: 4
Query Match: 66.96% Indels: 6
DB: 14 Gaps: 0
US-09-705-500A-3 (1-247) x BQ308414 (1-577)
Qy 38 AsnSerAlaGluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPhe 57
Db 1-AACTCAGCTGAAGTGGTTC--TGCTCAACAGTGTCTACAGTGGTGGGGGC-TTT 57
Qy 58 AlaCysLeuGluAsnSerThrCysAspThr-AspGlyMetTyrAspIleCysLysSerPh 77
Db 58 GCATGCTGGAAACTCCACCTGTGACACAGATGGGATGTATGACATCTGTAAATCCTT 117
Qy 77 GluTyrSerAlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLy 97
Db 118 CTGTGACAGCGCTGTAATTGACACCTCAGGAAAGACATTCGTCAAAGAGAGCTTAA 177
Qy 97 sCysIleAlaAsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPh 117
Db 178 ATGCATCGCCACGSGGTCACTCCAGAGTCTTCCTGCCATTCGAGGTGCTCCACTTT 237
Qy 117 eGlnArgMetIleAlaGluValGlnGluCysTyrSerLysLeuAsnValCysSerIle 137
Db 238 CCAAGAGATGATTGCTGAGGTGCAGGAAGAGTGTACAGCAAGCTGAATGTGTGAGCAT 297
Qy 137 eAlaLysArgAsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAs 157
Db 298 CGCCAAAGCGGACCTGAAGCCATCACTGAGTCTGTCAGTGCCTCAATCACTTCCAA 357
Qy 157 nArgTyrTrpAsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerTh 177
Db 358 CAGATCTATACACACTTGTCCGAAGCTGCTGGAATGTGTGAAGACACAGTCAGCAC 417
Qy 177 rIleArgAspSerLeuMetGluLysIleGlyPro-AsnMetAlaSerLeuPheHisIleL 197

Db 418 AATCAGACAGCCTGATGGAGAAATTTGGCCCTAAACATGCCAGCCTCTTCCACATCC 477
Qy 197 euGlnThrAspHisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgThrA 217
Db 478 TGCAGACAGACCACTGTGCCCAACACACACCCAGCAGTGTCTCAACAGAGAGACGCC 536
Qy 217 snGluProGlnLysLeuLysVal 224
Db 537 ATGAGCCGAA-AAGCTGAAAGTC 558
RESULT 12
BF042539
LOCUS BP250022A10G7 Soares normalized bovine placenta Bos taurus cDNA
DEFINITION clone BP250022A10G7 5', mRNA sequence.
ACCESSION BF042539
VERSION BF042539.1 GI:10759594
KEYWORDS EST.
SOURCE cow.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 560)
AUTHORS Lewin,H.A., Soares,M.B., Rebeiz,M., Pardinas,J., Liu,L. and Larson,
J.H.
TITLE Bovine ESTs
JOURNAL Unpublished (2000)
COMMENT Contact: Lewin, H. A.
W. M. Keck Center for Comparative and Functional Genomics
University of Illinois at Urbana-Champaign
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61801, USA
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Fax: 217 244 5617
Email: h-lewin@uiuc.edu
Funding for cattle EST sequencing was provided by the USDA National
Research Initiative, Animal Genome Resource Grant AG 99-3205-8534
to H. A. Lewin and J. E. Womack. Base Calling/Quality Scores: PHRED
from Washington University Genome Center. Vector Trimmi g:
Cross_match from Washington University Genome Center PHRAP suite.
This sequence is vector free and at least 200 bp in length.
PCR Primers
FORWARD: TAATACGACTCATATAGG
BACKWARD: ATTAACCTCCTACTAAAG
Insert Length: 560 Std Error: 0.00
Plate: BP250022A10 row: G column: 7
Seq primer: AGCGATAACAATTCACACAGGA
High quality sequence stop: 560.
Location/Qualifiers
1. .560
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="BP250022A10G7"
/sex="Female"
/lab_host="DH10B"
/note="Organ: placenta; Vector: p773Pac; Site 1: EcoRI;
Site 2: NotI; The cDNA library was contributed by the
Soares laboratory and it was constructed and normalized
as described by Bonaldo, M.F., Lennon, G. and Soares,
M.B. (1996), Genome Research 6(9): 791-806."

BASE COUNT 150 a 142 c 146 g 122 t
ORIGIN
Alignment Scores:
Pred. No.: 6,45e-94 Length: 560
Score: 848.00 Matches: 165
Percent Similarity: 99.41% Conservative: 4
Best Local Similarity: 97.06% Mismatches: 1
Query Match: 66.88% Indels: 0
DB: 12 Gaps: 0

JOURNAL Unpublished (2001)
COMMENT Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segre@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
source
1..908
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0D1058YD08"
/clone_lib="LTI NFL006 PL2"
/tissue_type="placenta"
/note="Vector: pCMVSPORT 6; Site 1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"

BASE COUNT 262 a 246 c 181 g 215 t 4 others
ORIGIN

Alignment Scores:
Pred. No.: 2,01e-92 Length: 908
Score: 839.00 Matches: 162
Percent Similarity: 98.18% Conservative: 0
Best Local Similarity: 98.18% Mismatches: 3
Query Match: 66.17% Indels: 0
DB: 9 Gaps: 0

US-09-705-500A-3 (1-247) x AL550611 (1-908)

Qy 83 LysPheAspThrGlnGlySerAlaPheValLysGluSerLeuLysCysIleAlaHsngly 102
Db 1 AAATTGTGACATCGAGGAAAGCATTCGTCAAGAGAGCTTAAATGTCATGCCAACCGG 60

Qy 103 ValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMetIleAla 122
Db 61 GTCACCTCCAGGTCTTCTCCGCTTCGGAGTGTCTCCACTTTCAAAGGATGATTGCT 120

Qy 123 GluValGlnGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArgAsnPro 142
Db 121 GAGGTGCAGGAAGAGTGCTACAGCAAGCTGAATGTGTGAGCATCGCCAAGCGGAACCT 180

Qy 143 GluAlaIleThrGluValGlnLeuProAsnHisPheSerAsnArgTyrTrzAsnArg 162
Db 181 GAAGCCATCAGTGGTCCGTCAGCTGCCCAATCACTTCTCCACAGATACTATTAACAGA 240

Qy 163 LeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAspSerLeu 182
Db 241 CTTGTCCGAGGCTGCGGAATGTGATGAGACACAGTCAGCAATCARAGACAGCCTG 300

Qy 183 MetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAspHisCys 202
Db 301 ATGGAGAAATATGGGCTTAACATGCGACCTCTTCCACATCTCAGACAGCACTGT 360

Qy 203 AlaGlnThrHisProArgNlaAspPheAsnArgArgThrAsnGluProGlnLysLeu 222
Db 361 GCCCAACACACACCCAGAGTCACTTCAACAGGAGACGCCCAATGAGCGCAGAAGCTG 420

Qy 223 LysValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHisIleLysArgThr 242
Db 421 AAAGTCTCTCTCAGGAACCTCCSAGGTGAGGAGGACTCTCCCTCCACATCAACGCACA 480

Qy 243 SerHisGluSerAla 247
Db 481 TCCCATGAGATGCA 495

RESULT 15
BM924595

LOCUS BM924595 1010 bp mRNA linear EST 12-MAR-2002
DEFINITION AGENCOURT 6767843 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5760977
5', mRNA sequence.
ACCESSION BM924595
VERSION BM924595.1 GI:19374974
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1010)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12808 Row: n column: 18
High quality sequence stop: 614.
FEATURES
source
1..1010
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5760977"
/clone_lib="NIH_MGC_116"
/lab_host="DH10B"
/note="Organ: pooled colon, kidney, stomach; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source anonymous pool of 3 colons, age 26 yo male, 49 yo female, 71 yo male colon; 46 yo male kidney, and pool of 2 stomachs, 62 yo male and 70 yo female. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 023. Note: this is a NIH MGC Library."

BASE COUNT 305 a 285 c 251 g 169 t
ORIGIN

Alignment Scores:
Pred. No.: 1,26e-89 Length: 1010
Score: 817.00 Matches: 183
Percent Similarity: 79.75% Conservative: 10
Best Local Similarity: 75.62% Mismatches: 22
Query Match: 64.43% Indels: 27
DB: 14 Gaps: 6

US-09-705-500A-3 (1-247) x BM924595 (1-1010)

Qy 1 MetLeuGlnAsnSerAlaValLeuValLeuValIleSerAlaSerAlaThrHisGlu 20
Db 263 ATGCTCCAAAACACTCAGCAGTGCTTCTGTGTGTGTGATCAGTCTTCTGCAACCATCAG 322

Qy 21 AlaGluGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
Db 323 GCGGAGCAGAAATGACTCTGTGAGCCCCAGGAAATCCCGAGTGGCGCTCAAACTCAGCT 382

Qy 41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
Db 383 GAAGTGGTTCGTTCCCTCAACAGTGTCTACAGTTCGCGCTCGGGGCTTTTTCATGCTGCT 442

Qy 61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
Db 443 GAAACCTCCACTGTGACACAGATGGGATGTATGACATCTGTAAATCTCTTTGTACAGC 502

Qy 81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAla 100

[illegible]

Search completed: June 12, 2003, 21:14:01
Job time : 1425 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 12, 2003, 17:27:49 ; Search time 60 Seconds
(without alignments)
548.548 Million cell updates/sec

Title: US-09-705-500A-3
Perfect score: 1268
Sequence: 1 MLQNSAVLLVLVISASATHE.....NLRGEDSPSHIKRTSHESA 247

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_101002.*
1: /SID52/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
2: /SID52/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
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22: /SID52/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SID52/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1268	100.0	247	16	Stanniocalcin from
2	1268	100.0	247	21	Human stanniocalcin
3	1268	100.0	247	21	Human stanniocalcin
4	1268	100.0	247	21	Human stanniocalcin
5	1268	100.0	247	21	Human stanniocalcin
6	1268	100.0	247	21	Human stanniocalcin
7	1268	100.0	247	22	Human stanniocalcin
8	1268	100.0	247	22	Human stanniocalcin
9	937	73.9	276	21	Human prostate can
10	680.5	53.7	261	9	Corpuscles of Stan

11	662.5	52.2	256	22	AA82474	Coho salmon stanni
12	628	49.5	170	21	AA55749	A. australis stann
13	358	28.2	70	22	AB31928	Peptide #4579 enco
14	358	28.2	70	22	AB31928	Peptide #4579 enco
15	358	28.2	70	22	AB31928	Peptide #4672 enco
16	358	28.2	70	22	AB31928	Peptide #4672 enco
17	358	28.2	70	22	AB31928	Human brain expres
18	358	28.2	70	22	AA70300	Human bone marrow
19	358	28.2	70	22	AA70300	Peptide #4568 enco
20	358	28.2	70	22	AA70300	Peptide #4674 enco
21	358	28.2	70	22	AA70300	Peptide #4445 enco
22	354.5	28.0	296	21	AA67926	Human peptide enco
23	354.5	28.0	296	22	AA67926	Mouse stanniocalci
24	354	27.9	293	20	AA41255	Murine stanniocalc
25	354	27.9	293	21	AA41255	Adipogenesis inhib
26	354	27.9	293	22	AA41255	Human adipocytogen
27	354	27.9	302	21	AA67925	Human stanniocalci
28	354	27.9	302	22	AA67925	Human stanniocalci
29	354	27.9	302	22	AA67925	Human adipogenesis
30	354	27.9	302	22	AA67925	Human protein sequ
31	354	27.9	302	22	AA67925	Amino acid sequenc
32	335.5	26.5	251	17	AA97978	Stanniocalcin alph
33	333.5	26.3	251	21	AA55748	Human stanniocalci
34	111	8.8	40	20	AA41254	Adipogenesis inhib
35	111	8.8	40	21	AA62687	N-terminal amino a
36	111	8.8	40	22	AA98970	Adipogenesis inhib
37	99	7.8	40	20	AA41253	Adipogenesis inhib
38	99	7.8	40	21	AA62687	N-terminal amino a
39	99	7.8	40	22	AA98969	Adipogenesis inhib
40	93	7.3	19	21	AA82531	Human stanniocalci
41	91	7.2	901	23	AA66003	P. patens cell cyc
42	90.5	7.1	783	23	AB35616	Fungal ZEC protein
43	90	7.1	282	20	AA02781	Human secreted pro
44	90	7.1	331	23	AB41192	Human ovarian anti
45	89.5	7.1	10182	23	ABP38314	Staphylococcus epi

ALIGNMENTS

RESULT 1

AA84522	AA84522 standard; Protein; 247 AA.	
ID	AA84522 standard; Protein; 247 AA.	
XX		
AC	AA84522;	
XX		
DT	19-APR-1996 (first entry)	
XX		
DE	Stanniocalcin from Corpuscles of Stannius.	
XX		
KW	stanniocalcin; Corpuscles of Stannius; hypocalcaemia; hypercalcaemia;	
KW	electrolyte disorder; osteoporosis; Paget's disease; treatment.	
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	Region	1..33
FT	Protein	/label= prepro_region
FT		34..247
XX		/label= mature_stanniocalcin
PN	WO9524411-A1.	
XX		
PD	14-SEP-1995.	
XX		
PF	09-MAY-1994; 94WO-US05136.	
XX		
PR	08-MAR-1994; 94US-0208005.	
XX		
PA	(HUMA-) HUMAN GENOME SCI INC.	
XX		
PI	Adams MD, Olsen H;	
XX		

DR WPI; 1995-328227/42.
 DR N-PSDB; AAT02438.
 XX Human corpuscles of Stannius polypeptide(s) - used to treat
 PT hypercalcaemia, hypocalcaemia and other electrolyte disorders
 XX Claim 14; Fig 1; 4lpp; English.
 XX Stanniocalcin, a Corpuscles of Stannius polypeptide is encoded by
 CC AAT02438. Stanniocalcin functions as a hypocalcaemic agent, and can be
 CC used for the treatment of e.g. electrolyte disorders which lead to renal,
 CC bone and heart diseases, hypertension, hypercalcaemia and disorders due
 CC to elevated bone resorption, e.g. osteoporosis and Paget's disease.
 XX Sequence 247 AA;
 SQ Query Match 100.0%; Score 1268; DB 16; Length 247;
 Best Local Similarity 100.0%; Pred. No. 5.9e-124; Mismatches 0; Indels 0; Gaps 0;
 Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLQNSAVLLVLVISASATHEAEQNDSPKSRVAAQNSAEVVRCLNSALQVGCFAFACL 60
 DB 1 MLQNSAVLLVLVISASATHEAEQNDSPKSRVAAQNSAEVVRCLNSALQVGCFAFACL 60
 QY 61 ENSTCDTGMVDICKSFLYSAAKFTQGFVKSFKCIANGVTSKVFLAIRRCSTFORM 120
 DB 61 ENSTCDTGMVDICKSFLYSAAKFTQGFVKSFKCIANGVTSKVFLAIRRCSTFORM 120
 QY 121 IAEVQEECYSKLVNCSIAKRNPETAEVQVLPNHFNSRYNRLVRSLLCEDDTVTIRD 180
 DB 121 IAEVQEECYSKLVNCSIAKRNPETAEVQVLPNHFNSRYNRLVRSLLCEDDTVTIRD 180
 QY 181 SLMEKIGPNMASLFILOTHCAQTHPRADFNRRRTNEPQKLKVLRLNRGEEDSPSHIK 240
 DB 181 SLMEKIGPNMASLFILOTHCAQTHPRADFNRRRTNEPQKLKVLRLNRGEEDSPSHIK 240
 QY 241 RTSHEA 247
 DB 241 RTSHEA 247
 RESULT 2
 ID AAB23264 standard; Protein; 247 AA.
 AC AAB23264;
 DT 02-FEB-2001 (first entry)
 DE Human stanniocalcin.
 KW Human; stanniocalcin; STC; osteogenesis; bone disease; osteoporosis;
 KW mineral metabolism regulator; prophylaxis; therapy.
 OS Homo sapiens.
 PN JP2000229880-A.
 PD 22-AUG-2000.
 PF 10-FEB-1999; 99JP-0033262.
 PR 10-FEB-1999; 99JP-0033262.
 PA (SNOW) SNOW BRAND MILK PROD CO LTD.
 XX WPI; 2000-605236/58.
 DR N-PSDB; AAA97594.
 XX An osteogenesis promoter useful in the prevention and/or treatment of
 PT bone diseases such as osteoporosis -
 XX Example 1; Page 5-6; 6pp; Japanese.

XX The invention relates to a novel osteogenesis-promoting composition
 CC which contains stanniocalcin (STC) as the active component.
 CC Stanniocalcin is a possible regulator of mineral metabolism. The
 CC composition is useful as a prophylactic and/or therapeutic agent for
 CC bone diseases such as osteoporosis. The present sequence represents
 CC human stanniocalcin which was used in an exemplification of the
 CC invention.
 XX Sequence 247 AA;
 SQ Query Match 100.0%; Score 1268; DB 21; Length 247;
 Best Local Similarity 100.0%; Pred. No. 5.9e-124; Mismatches 0; Indels 0; Gaps 0;
 Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLQNSAVLLVLVISASATHEAEQNDSPKSRVAAQNSAEVVRCLNSALQVGCFAFACL 60
 DB 1 MLQNSAVLLVLVISASATHEAEQNDSPKSRVAAQNSAEVVRCLNSALQVGCFAFACL 60
 QY 61 ENSTCDTGMVDICKSFLYSAAKFTQGFVKSFKCIANGVTSKVFLAIRRCSTFORM 120
 DB 61 ENSTCDTGMVDICKSFLYSAAKFTQGFVKSFKCIANGVTSKVFLAIRRCSTFORM 120
 QY 121 IAEVQEECYSKLVNCSIAKRNPETAEVQVLPNHFNSRYNRLVRSLLCEDDTVTIRD 180
 DB 121 IAEVQEECYSKLVNCSIAKRNPETAEVQVLPNHFNSRYNRLVRSLLCEDDTVTIRD 180
 QY 181 SLMEKIGPNMASLFILOTHCAQTHPRADFNRRRTNEPQKLKVLRLNRGEEDSPSHIK 240
 DB 181 SLMEKIGPNMASLFILOTHCAQTHPRADFNRRRTNEPQKLKVLRLNRGEEDSPSHIK 240
 QY 241 RTSHEA 247
 DB 241 RTSHEA 247
 RESULT 3
 ID AAY92901 standard; Protein; 247 AA.
 AC AAY92901;
 DT 26-SEP-2000 (first entry)
 DE Human stanniocalcin protein.
 KW PCR primer; human; stanniocalcin; inhibitor; differentiation; maturation;
 KW adipocyte; obesity; diabetes; hypertension; heart disease.
 OS Homo sapiens.
 PN WO200016795-A1.
 PD 30-MAR-2000.
 PF 17-SEP-1999; 99WO-JP05080.
 PR 17-SEP-1998; 98JP-0263004.
 XX (SNOW) SNOW BRAND MILK PROD CO LTD.
 PA Goto M, Tomoyasu A, Yamaguchi K, Kinoshita M, Nakagawa N;
 PI WPI; 2000-283445/24.
 DR N-PSDB; AAA11145.
 XX Treating or preventing obesity, which is a risk factor for diabetes,
 PT hypertension and heart disease, comprises administering an agent
 PT containing stanniocalcin -
 XX Example 1; Page 16; 19pp; Japanese.
 XX This sequence represents the human stanniocalcin protein. Stanniocalcin

CC is an inhibitor of the differentiation and maturation of adipocytes. The
 CC protein is used for preventing and treating obesity which is a risk
 CC factor for diabetes, hypertension, and heart disease. The coding sequence
 CC was isolated from IMR-90 cells.

XX Sequence 247 AA;

Query Match 100.0%; Score 1268; DB 21; Length 247;

Best Local Similarity 100.0%; Pred. No. 5.9e-124;
 Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQNSAVLLVLVISASATHEAEQNDSPKSRVAAQNSAEVVRCLNSALQVCGGAFACL 60

DB 1 MLQNSAVLLVLVISASATHEAEQNDSPKSRVAAQNSAEVVRCLNSALQVCGGAFACL 60

QY 61 ENSTCDTGMVDICKSFYSAKFTQGFVKSLEKCIANGVTSKVFIAIRRCSTFORM 120

DB 61 ENSTCDTGMVDICKSFYSAKFTQGFVKSLEKCIANGVTSKVFIAIRRCSTFORM 120

QY 121 IAEVQEECYKLVCSIAKRNPEAITEVVQLPNHFNSRYNRLVRSLLCEDEDTVSTIRD 180

DB 121 IAEVQEECYKLVCSIAKRNPEAITEVVQLPNHFNSRYNRLVRSLLCEDEDTVSTIRD 180

QY 181 SLMEKIGPNMASLPHILOTDHCAQTHPRADFNRRRTNEPQKLKVLRLNRGEEDSPSHIK 240

DB 181 SLMEKIGPNMASLPHILOTDHCAQTHPRADFNRRRTNEPQKLKVLRLNRGEEDSPSHIK 240

QY 241 RTSHESA 247

DB 241 RTSHESA 247

RESULT 4

AAV55750

ID AAV55750 standard; Protein; 247 AA.

XX AC AAV55750;

XX 11-FEB-2000 (first entry)

DE Human stanniocalcin polypeptide.

XX Stanniocalcin-alpha polypeptide; teleocalcin; hypocalcin; hypocalcemic;

KW anti-hypercalcemic glycoprotein hormone; corpuscles of stannius; PTH;

KW parathyroid hormone; bone reabsorption; osteoporosis; gene therapy; bone;

KW electrolyte disorder; renal; heart disease; osteopetrosis; human;

KW Paget's disease; hypercalcemia.

XX OS Homo sapiens.

XX US5994103-A.

XX 30-NOV-1999.

XX 02-JUN-1995; 95US-0460529.

XX 10-NOV-1994; 94WO-US13206.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Fleischmann RD, Olsen HS;

XX WPI; 2000-038260/03.

XX Isolated nucleic acids encoding human stanniocalcin-alpha useful for

PT treating electrolyte disorders which lead to renal, bone and heart

PT diseases, osteoporosis and Paget's disease -

XX Disclosure; Fig 3; 21pp; English.

XX The invention provides a human stanniocalcin-alpha polypeptide (also

CC called teleocalcin and hypocalcin). Stanniocalcin-alpha is an anti-

CC hypercalcemic glycoprotein hormone produced by the corpuscles of

CC stannius. It has a similar reported biological activity to that of
 CC parathyroid hormone (PTH) and both these proteins exhibit dual functions
 CC in mammals. They exert hypercalcemic activity due to stimulation of bone
 CC reabsorption. Further PTH has a biphasic action on bone metabolism (i.e.
 CC at low doses it increases bone formation and at high doses it increases
 CC bone reabsorption. Accordingly, human stanniocalcin-alpha and antagonists
 CC of it (under different circumstances) may be used to treat osteoporosis.
 CC The DNA may be used to produce human stanniocalcin-alpha according to
 CC standard recombinant DNA methodologies. The human stanniocalcin-alpha may
 CC be produced either in vitro in a fermentation culture or in vivo as part
 CC of a gene therapy protocol, and may be used to treat electrolyte
 CC disorders which lead to renal, bone and heart diseases. Due to the
 CC biphasic nature of stanniocalcin-alpha it may be used to treat
 CC osteoporosis, osteopetrosis and Paget's disease. Alternatively, the
 CC polypeptides may be used as antigens in the production of antibodies to
 CC stanniocalcin-alpha and to assay for agonists and antagonists of its
 CC activity. The antibodies and antagonists may be used to inhibit the
 CC activity of stanniocalcin-alpha and may be used to treat osteoporosis and
 CC hypercalcemia. The present sequence represents a human stanniocalcin.

XX Sequence 247 AA;

Query Match 100.0%; Score 1268; DB 21; Length 247;

Best Local Similarity 100.0%; Pred. No. 5.9e-124;
 Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQNSAVLLVLVISASATHEAEQNDSPKSRVAAQNSAEVVRCLNSALQVCGGAFACL 60

DB 1 MLQNSAVLLVLVISASATHEAEQNDSPKSRVAAQNSAEVVRCLNSALQVCGGAFACL 60

QY 61 ENSTCDTGMVDICKSFYSAKFTQGFVKSLEKCIANGVTSKVFIAIRRCSTFORM 120

DB 61 ENSTCDTGMVDICKSFYSAKFTQGFVKSLEKCIANGVTSKVFIAIRRCSTFORM 120

QY 121 IAEVQEECYKLVCSIAKRNPEAITEVVQLPNHFNSRYNRLVRSLLCEDEDTVSTIRD 180

DB 121 IAEVQEECYKLVCSIAKRNPEAITEVVQLPNHFNSRYNRLVRSLLCEDEDTVSTIRD 180

QY 181 SLMEKIGPNMASLPHILOTDHCAQTHPRADFNRRRTNEPQKLKVLRLNRGEEDSPSHIK 240

DB 181 SLMEKIGPNMASLPHILOTDHCAQTHPRADFNRRRTNEPQKLKVLRLNRGEEDSPSHIK 240

QY 241 RTSHESA 247

DB 241 RTSHESA 247

RESULT 5

AAV57166

ID AAV57166 standard; Protein; 247 AA.

XX AC AAV57166;

XX 11-FEB-2000 (first entry)

XX Human corpuscles of stannius polypeptide.

XX Corpuscles of stannius polypeptide; calcium; inhibition; human; renal;

XX therapeutic; bone; heart disease; hypocalcemia; osteoporosis.

XX OS Homo sapiens.

XX US5994301-A.

XX 30-NOV-1999.

XX 28-APR-1995; 95US-0431117.

XX 08-MAR-1994; 94US-0208005.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Adams MD, Olsen HS;

XX WPI; 2000-038269/03.
 DR N-PSDB; AAZ39520.
 XX
 PT Human corpuscles of stanius polypeptides used to inhibit calcium uptake
 PT
 PS Claim 4; Fig 1A-B; 23pp; English.
 XX
 CC This represents a human corpuscles of stanius polypeptide, having a
 CC calcium uptake inhibitory activity. The cDNA is deposited under the
 CC accession number ATCC Deposit No. 75652. The polypeptide can be used in a
 CC method for the treatment of a patient having need to inhibit uptake of
 CC calcium. The method is also used for the therapeutic treatment of renal,
 CC bone, and heart diseases, and the antagonist (may be an antibody) may be
 CC used for treating hypocalcemia, and osteoporosis.
 XX
 SQ Sequence 247 AA;
 Query Match 100.0%; Score 1268; DB 21; Length 247;
 Best Local Similarity 100.0%; Pred. No. 5.9e-124;
 Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLQNSAVLLVVISASATHEAEQNDVSVPKSRVAAQNSAEVVRCLNSALQVCGCAFACL 60
 Db 1 MLQNSAVLLVVISASATHEAEQNDVSVPKSRVAAQNSAEVVRCLNSALQVCGCAFACL 60
 QY 61 ENSTCDTDGMYDICKSFYLSAAKFTQGAFFVKESLKCIANGVTSKVFLAIRRCSSTFORM 120
 Db 61 ENSTCDTDGMYDICKSFYLSAAKFTQGAFFVKESLKCIANGVTSKVFLAIRRCSSTFORM 120
 QY 121 IAEVQECYKLVNCSIAKRNPPEAITEVQLPNHFSNRYNRLVRSLLCEDETVSTIRD 180
 Db 121 IAEVQECYKLVNCSIAKRNPPEAITEVQLPNHFSNRYNRLVRSLLCEDETVSTIRD 180
 QY 181 SLMEKIGPNMASLPHILOTHCAQTHPRADFNRRRTNEPQKLKVLRLNRGEEDESPSHIK 240
 Db 181 SLMEKIGPNMASLPHILOTHCAQTHPRADFNRRRTNEPQKLKVLRLNRGEEDESPSHIK 240
 QY 241 RTSHESA 247
 Db 241 RTSHESA 247
 RESULT 6
 AAB62690 standard; Protein; 247 AA.
 XX
 AC AAB62690;
 XX
 DT 06-AUG-2001 (first entry)
 XX
 DE Lng108, a diagnostic marker for cancer.
 XX
 KW Lng108; cancer; diagnostic marker; cytotoxic; immune response; imaging.
 XX
 OS Homo sapiens.
 XX
 PN WO200132209-A1.
 XX
 PD 10-MAY-2001.
 XX
 PF 03-NOV-2000; 2000WO-US30482.
 XX
 PR 04-NOV-1999; 99US-0163444.
 XX
 PA (DIAD-) DIADEXUS INC.
 XX
 PI Recipon H, Macina RA, Chen S, Sun Y;
 XX
 DR WPI; 2001-316386/33.
 DR N-PSDB; AAF83823.
 XX

PT Novel assay for diagnosing and monitoring cancer, involves determining
 PT levels of Lng108 in cells, tissues or bodily fluids of the patient, and
 PT comparing with control -
 XX
 PS Disclosure; Page 33-34; 36pp; English.
 XX
 CC The invention relates to diagnosing the presence of cancer or diagnosing
 CC metastases of cancer in a patient that involves determining levels of
 CC Lng108 in a sample of cells, tissues or bodily fluids in a patient, and
 CC comparing the determined levels with levels of Lng108 in a normal human
 CC control. The method is useful for diagnosing the presence of cancer,
 CC diagnosing metastases of cancer, staging cancer, monitoring cancer, and
 CC monitoring a change in stage of the cancer, in a patient. A therapeutic
 CC agent which is an antibody labeled with paramagnetic ions or a
 CC radioisotope, and conjugated with a cytotoxic agent is useful for imaging
 CC cancer in a patient. A molecule which downregulates the expression or
 CC activity of Lng108, is useful for treating cancer in a patient. Lng108
 CC protein is useful for inducing an immune response against a target cell
 CC expressing Lng108. The present sequence represents the human Lng108
 CC polypeptide.
 XX
 SQ Sequence 247 AA;
 Query Match 100.0%; Score 1268; DB 22; Length 247;
 Best Local Similarity 100.0%; Pred. No. 5.9e-124;
 Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLQNSAVLLVVISASATHEAEQNDVSVPKSRVAAQNSAEVVRCLNSALQVCGCAFACL 60
 Db 1 MLQNSAVLLVVISASATHEAEQNDVSVPKSRVAAQNSAEVVRCLNSALQVCGCAFACL 60
 QY 61 ENSTCDTDGMYDICKSFYLSAAKFTQGAFFVKESLKCIANGVTSKVFLAIRRCSSTFORM 120
 Db 61 ENSTCDTDGMYDICKSFYLSAAKFTQGAFFVKESLKCIANGVTSKVFLAIRRCSSTFORM 120
 QY 121 IAEVQECYKLVNCSIAKRNPPEAITEVQLPNHFSNRYNRLVRSLLCEDETVSTIRD 180
 Db 121 IAEVQECYKLVNCSIAKRNPPEAITEVQLPNHFSNRYNRLVRSLLCEDETVSTIRD 180
 QY 181 SLMEKIGPNMASLPHILOTHCAQTHPRADFNRRRTNEPQKLKVLRLNRGEEDESPSHIK 240
 Db 181 SLMEKIGPNMASLPHILOTHCAQTHPRADFNRRRTNEPQKLKVLRLNRGEEDESPSHIK 240
 QY 241 RTSHESA 247
 Db 241 RTSHESA 247
 RESULT 7
 AAB62473 standard; Protein; 247 AA.
 XX
 AC AAB62473;
 XX
 DT 09-JUL-2001 (first entry)
 XX
 DE Human stanniocalcin (STC) protein.
 XX
 KW Stanniocalcin; STC; neuroprotective; antiinflammatory; antianemic;
 KW antirheumatic; antiarthritic; dermatological; antiallergic; human;
 KW nephrotropic; antithyroid; immunosuppressive; antidiabetic; vulnerary;
 KW antiasthmatic; hemostatic; antiarrhythmic; vasotropic; antipsoriatic;
 KW antitumor; anti HIV; antiparkinsonian; nootropic; cell proliferation;
 KW hemostatic; thrombolytic.
 XX
 OS Homo sapiens.
 XX
 PN WO200130969-A2.
 XX
 PD 03-MAY-2001.
 XX
 PF 20-OCT-2000; 2000WO-US29432.
 XX

PR 27-OCT-1999; 99US-0161740.
XX (HUMA-) HUMAN GENOME SCI INC.
PA (UYHE-) UNIV HELSINKI.
XX
XX Olsen HS, Zhang K, Lindeberg P, Tatlisumak T, Kaste M;
PI Andersson LC;
XX WPI; 2001-308626/32.
DR N-PSDB; AAF83297.
XX
XX Novel composition useful for treating or protecting neural cells, for
PT treating Addison's disease, organ rejection, hyperproliferative
PT disorder, cancer, AIDS, multiple sclerosis, comprises stanniocalcin
PT polypeptide -
XX
PS Claim 1; Fig 1A-C; 253pp; English.
XX
XX The invention relates to a human stanniocalcin (STC) polypeptide. A
CC pharmaceutical composition comprising the STC is useful for treating a
CC patient in need of increased levels of STC activity. STC and its
CC modulators are useful for treating disorders or abnormalities of nervous
CC system, cerebrovascular diseases, dementia, encephalitis, central
CC nervous system infections or neoplasms, demyelinating diseases,
CC encephalomyelitis, spinal cord diseases, mental retardation such as
CC Down's syndrome, Tay-Sachs disease, neuromuscular diseases such as
CC muscular dystrophy, myasthenia gravis, deficiencies or disorders of
CC immune system such as Addison's disease, hemolytic anemia, rheumatoid
CC arthritis, dermatitis, glomerulonephritis, Goodpasture's Syndrome,
CC Grave's disease, multiple sclerosis, autoimmune thyroiditis, systemic
CC lupus erythematosus, insulin dependent diabetes mellitus, allergic
CC reactions and conditions such as asthma, for treating and/or preventing
CC organ rejection or graft-versus-host disease, hyperproliferative diseases
CC such as purpura, Gaucher's disease, cardiovascular disorders such as
CC arrhythmias, telangiectasia, vasculitis, and for treatment of disease or
CC disorders with neovascularization. The composition can be used to treat
CC hemangioma, psoriasis, angiofibroma, atherosclerotic plaques, delayed
CC wound healing, granulations, Osler-Weber syndrome, solid tumors such as
CC Kaposi's sarcoma, cancer, AIDS, neurodegenerative disorders such as
CC Alzheimer's disease, Parkinson's disease, wound healing, and for treating
CC or detecting infectious agents. The present sequence represents the
CC human STC polypeptide.
XX
SQ Sequence 247 AA;
Query Match 100.0%; Score 1268; DB 22; Length 247;
Best Local Similarity 100.0%; Pred. No. 5.9e-124;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLQNSAVLLVLVISASATHEAEQNDVSVPKRSRVAQAQNSAEVVRCLNSALQVGCAPACL 60
DB 1 MLQNSAVLLVLVISASATHEAEQNDVSVPKRSRVAQAQNSAEVVRCLNSALQVGCAPACL 60
QY 61 ENSTCDTGMVDICKSFLYSAAKFTQKAFVKESLKCIAANGVTSKVFLAIRRCSSTFORM 120
DB 61 ENSTCDTGMVDICKSFLYSAAKFTQKAFVKESLKCIAANGVTSKVFLAIRRCSSTFORM 120
QY 121 IAEVQEECYKLNVCISIAKRNPETAEVQLPNHFNSRNYNRLVRSLLCEDDTVSTIRD 180
DB 121 IAEVQEECYKLNVCISIAKRNPETAEVQLPNHFNSRNYNRLVRSLLCEDDTVSTIRD 180
QY 181 SLMEKIGPNMASLPHILOTHCAQTHPRADFNRRRTNEPQKLKVLRLNLRGEEDSPSHIK 240
DB 181 SLMEKIGPNMASLPHILOTHCAQTHPRADFNRRRTNEPQKLKVLRLNLRGEEDSPSHIK 240
QY 241 RTSHEA 247
DB 241 RTSHEA 247

RESULT 8
ABB06259
ID ABB06259 standard; Protein; 247 AA.

XX ABB06259;
XX 23-MAY-2002 (first entry)
XX Human stanniocalcin 1 protein.
XX
XX Human; stanniocalcin 1; osteopathic; osteogenesis failure; osteoporosis;
KW bone mass reduction; traumatic bone injury; osteomalacia; bone disease;
KW rheumatic bone disease; cancer associated bone disease; rachitis;
KW arthritis deformans.
XX
OS Homo sapiens.
XX WO200204013-A1.
XX 17-JAN-2002.
XX 10-JUL-2001; 2001WO-JP05962.
XX 11-JUL-2000; 2000JP-0209926.
XX (BMLB-) BML INC.
XX Yoshihiko Y, Koide Y, Igarashi A, Takano S, Maeda N, Aubin JB;
PI WPI; 2002-164600/21.
XX N-PSDB; ABL40225.
XX Agent used for treating bone diseases e.g. osteoporosis, traumatic bone
PT injury, osteomalacia, rheumatic bone diseases, bone diseases associated
PT with cancer and arthritis deformans containing stanniocalcin 1 -
XX Claim 2; Fig 1; 24pp; Japanese.
XX The present invention describes an agent containing stanniocalcin 1,
CC particularly of human origin. Stanniocalcin 1 has osteopathic activity.
CC The agent can be used for treating diseases relating to osteogenesis
CC failure or reduction in bone mass e.g. osteoporosis, traumatic bone
CC injury, osteomalacia, rheumatic bone diseases, bone diseases associated
CC with cancer, bone diseases due to phosphorus or calcium metabolic error,
CC rachitis and arthritis deformans. The agent increases bone mass. The
CC present sequence represents human stanniocalcin 1.
XX
SQ Sequence 247 AA;
Query Match 100.0%; Score 1268; DB 23; Length 247;
Best Local Similarity 100.0%; Pred. No. 5.9e-124;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLQNSAVLLVLVISASATHEAEQNDVSVPKRSRVAQAQNSAEVVRCLNSALQVGCAPACL 60
DB 1 MLQNSAVLLVLVISASATHEAEQNDVSVPKRSRVAQAQNSAEVVRCLNSALQVGCAPACL 60
QY 61 ENSTCDTGMVDICKSFLYSAAKFTQKAFVKESLKCIAANGVTSKVFLAIRRCSSTFORM 120
DB 61 ENSTCDTGMVDICKSFLYSAAKFTQKAFVKESLKCIAANGVTSKVFLAIRRCSSTFORM 120
QY 121 IAEVQEECYKLNVCISIAKRNPETAEVQLPNHFNSRNYNRLVRSLLCEDDTVSTIRD 180
DB 121 IAEVQEECYKLNVCISIAKRNPETAEVQLPNHFNSRNYNRLVRSLLCEDDTVSTIRD 180
QY 181 SLMEKIGPNMASLPHILOTHCAQTHPRADFNRRRTNEPQKLKVLRLNLRGEEDSPSHIK 240
DB 181 SLMEKIGPNMASLPHILOTHCAQTHPRADFNRRRTNEPQKLKVLRLNLRGEEDSPSHIK 240
QY 241 RTSHEA 247
DB 241 RTSHEA 247

RESULT 9
AAB56848

ID AAB56848 standard; Protein; 276 AA.
 AC AAB56848;
 XX
 XX
 DT 13-MAR-2001 (first entry)
 DE Human prostate cancer antigen protein sequence SEQ ID NO:1426.
 XX
 XX
 KW Human; prostate cancer; prostate cancer antigen; detection; diagnosis;
 KW neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular;
 KW vulnary; gastrointestinal; nephrotropic; antinefactive; gynaecological;
 KW antibacterial; gene therapy; neural; immune; reproductive; renal;
 KW gastrointestinal; pulmonary; cardiovascular; proliferative disorder;
 KW wound; infectious disease.
 XX
 XX Homo sapiens.
 OS
 XX WO200055174-A1.
 PN
 XX
 XX 21-SEP-2000.
 PD
 XX
 XX 08-MAR-2000; 2000WO-US05988.
 PF
 XX 12-MAR-1999; 99US-0124270.
 PR
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA (ROSE/) ROSEN C.A.
 XX
 XX Rosen CA, Ruben SM;
 PI
 XX WPI; 2000-587513/55.
 DR N-PSDB; AAF16051.
 XX
 XX Prostate cancer associated gene sequences, referred to as prostate
 PT cancer antigens, useful for treatment, prevention, and diagnosis of
 PT disorders such as prostate cancer -
 PT
 XX Claim 11; Page 1858-1859; 2338pp; English.
 PS
 XX AAF15566 to AAF16505 encode the human prostate cancer associated
 CC proteins, called prostate cancer antigens, given in AAB56363 to AAB57302.
 CC The prostate cancer antigens can have neuroprotective, cytostatic,
 CC cardioactive, immunomodulatory, muscular, vulnary, gastrointestinal,
 CC nephrotropic, antinefactive, gynaecological and antibacterial activities,
 CC and can be used in gene therapy. The prostate cancer antigen
 CC polynucleotides may be used for detection of prostate cancer, chromosome
 CC identification, as chromosome markers, and for numerous other diagnostic
 CC or research purposes. The prostate cancer antigens may be used to treat
 CC disorders such as neural, immune, muscular, reproductive,
 CC gastrointestinal, pulmonary, cardiovascular, renal, and proliferative
 CC disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to
 CC AAB57303 represent sequences used in the exemplification of the present
 CC invention.
 XX
 XX
 SQ Sequence 276 AA;
 Query Match 73.9%; Score 937; DB 21; Length 276;
 Best Local Similarity 99.5%; Pred. No. 2.6e-89;
 Matches 185; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MLQNSAVLLVLVISASATHEAQNDVSVPKRSRVAQAQNSAEVVRCLNSALQVCGCAFACL 60
 DB 89 MLQNSAVLLVLVISASATHEAQNDVSVPKRSRVAQAQNSAEVVRCLNSALQVCGCAFACL 148
 QY 61 ENSTCDTGMVDICKSFLYSAKFTQKAFVKESLKIANGVTSKVFLAIRRCSFTFORM 120
 DB 149 ENSTCDTGMVDICKSFLYSAKFTQKAFVKESLKIANGVTSKVFLAIRRCSFTFORM 208
 QY 121 IAEVQECYKLVNCSIAKRNPEAITVQVLPNHFNSRYNRLVRSLLCEDEDTVTSTIRD 180
 DB 209 IAEVQECYKLVNCSIAKRNPEAITVQVLPNHFNSRYNRLVRSLLCEDEDTVTSTIRD 268
 QY 181 SLMEKI 186

Db 269 SLMEKI 274
 RESULT 10
 AAF82968
 ID AAF82968 standard; protein; 261 AA.
 XX
 AC AAF82968;
 XX
 DT 30-NOV-1990 (first entry)
 DE Corpuscles of Stannius CS protein precursor.
 XX
 KW Corpuscles of Stannius; CS protein; cardiovascular disease;
 KW oedema; heart failure; high blood pressure.
 XX
 OS Anguilla australis.
 XX
 XX Key Location/Qualifiers
 FT Peptide 1..17
 FT /label=signal peptide/prohormone
 FT Peptide 18..288
 FT /label=pro-CS
 XX
 PN WO8803949-A.
 XX
 PD 02-JUN-1988.
 XX
 XX 19-NOV-1987; 87WO-AU00389.
 PF
 XX 22-MAY-1987; 87AU-0002086.
 PR
 XX 22-MAY-1987; 87AU-0009107.
 XX
 XX (FLOR-) FLOREY INST EXPR.
 PA
 XX Butkus A, Coghlan JP, Roche PJ;
 PI
 XX WPI; 1988-161619/23.
 DR N-PSDB; AAN80655.
 XX
 XX CS protein of corpuscles of stannius - used for treating cardiovascular
 PT disease, renal disease and electrolyte disorders.
 PT
 XX Disclosure; ; p; English.
 PS
 XX This prepro-CS protein sequence has its signal or pro-hormone fragment
 CC (amino acids -17 to 1) cleaved to yield the pro-CS form which can be
 CC processed to yield the mature form. Recombinant DNA methods are
 CC utilised in the prodn. of the CS protein. It is useful as e.g. a
 CC therapeutic agent for the treatment of cardiovascular disease
 CC and oedema. See also AAN80654.
 CC
 XX SQ Sequence 261 AA;
 Query Match 53.7%; Score 680.5; DB 9; Length 261;
 Best Local Similarity 61.4%; Pred. No. 1.5e-62;
 Matches 124; Conservative 41; Mismatches 36; Indels 1; Gaps 1;
 QY 1 MLQNSAVLLVLVISASATHEAQNDVSVPKRSRVAQAQNSAEVVRCLNSALQVCGCAFACL 60
 DB 1 MLQNSAVLLVLVISASATHEAQNDVSVPKRSRVAQAQNSAEVVRCLNSALQVCGCAFACL 59
 QY 61 ENSTCDTGMVDICKSFLYSAKFTQKAFVKESLKIANGVTSKVFLAIRRCSFTFORM 120
 DB 60 DNSTCDTGMVDICKSFLYSAKFTQKAFVKESLKIANGVTSKVFLAIRRCSFTFORM 119
 QY 121 IAEVQECYKLVNCSIAKRNPEAITVQVLPNHFNSRYNRLVRSLLCEDEDTVTSTIRD 180
 DB 120 IAEVQECYKLVNCSIAKRNPEAITVQVLPNHFNSRYNRLVRSLLCEDEDTVTSTIRD 179
 QY 181 SLMEKIGPNMASLFILOTDHC 202

Db 180 GLVSRLEPMGVLFQLLTQKAC 201

RESULT 11

AA62474

ID AAB62474 standard; Protein; 256 AA.

XX AAB62474;

AC AAB62474;

XX 09-JUL-2001 (first entry)

XX Coho salmon stanniocalcin protein.

XX Stanniocalcin; STC; neuroprotective; antiinflammatory; antianemic;

KW antirheumatic; antiarthritic; dermatological; antiatherogenic; human;

KW nephrotropic; antithyroid; immunosuppressive; antidiabetic; vulnerary;

KW antiaschmatic; antiaerhythmic; antiaerhythmic; vasotropic; antipsoriatic;

KW antitumor; anti HIV; antiparkinsonian; nootropic; cell proliferation;

KW hemostatic; thrombolytic; coho salmon.

XX Oncoerhynchus kisutch.

OS WO200130969-A2.

XX 03-MAY-2001.

XX 20-OCT-2000; 2000WO-US29432.

XX 27-OCT-1999; 99US-0161740.

XX (HUMA-) HUMAN GENOME SCI INC.

PA (UYHE-) UNIV HELSINKI.

PI Olsen HS, Zhang K, Lindsberg P, Tatlisumak T, Kaste M;

PI Andersson LC;

XX WPI; 2001-308626/32.

XX Novel composition useful for treating or protecting neural cells, for

PT treating Addison's disease, organ rejection, hyperproliferative

PT disorder, cancer, AIDS, multiple sclerosis, comprises stanniocalcin

PT polypeptide -

PS Disclosure; Fig 2; 253pp; English.

XX The invention relates to a human stanniocalcin (STC) polypeptide. A

CC pharmaceutical composition comprising the STC is useful for treating a

CC patient in need of increased levels of STC activity. STC and its

CC modulators are useful for treating disorders or abnormalities of nervous

CC system, cerebrovascular diseases, dementia, encephalitis, central

CC nervous system infections or neoplasms, demyelinating diseases,

CC encephalomyelitis, spinal cord diseases, mental retardation such as

CC Down's syndrome, Tay-Sachs disease, neuromuscular diseases such as

CC muscular dystrophy, myasthenia gravis, deficiencies or disorders of

CC immune system such as Addison's disease, hemolytic anemia, rheumatoid

CC arthritis, dermatitis, glomerulonephritis, Goodpasture's Syndrome,

CC Grave's disease, multiple sclerosis, autoimmune thyroiditis, systemic

CC lupus erythematosus, insulin dependent diabetes mellitus, allergic

CC reactions and conditions such as asthma, for treating and/or preventing

CC organ rejection or graft-versus-host disease, hyperproliferative diseases

CC such as psoriasis, Gaucher's disease, cardiovascular disorders such as

CC arrhythmias, telangiectasia, vasculitis, and for treatment of disease or

CC disorders with neovascularization. The composition can be used to treat

CC hemangioma, psoriasis, angiodysplasia, atherosclerotic plaques, delayed

CC wound healing, granulomas, Ocular-Weber syndrome, solid tumors such as

CC Kaposi's sarcoma, cancer, AIDS, neurodegenerative disorders such as

CC Alzheimer's disease, Parkinson's disease, wound healing, and for treating

CC or detecting infectious agents. The present sequence represents the

CC coho salmon stanniocalcin protein, used in homology studies with the

XX human STC polypeptide.

XX Sequence 256 AA;

Query Match 52.2%; Score 662.5; DB 22; Length 256;

Best Local Similarity 53.4%; Pred. No. 1.1e-60;

Matches 125; Conservative 46; Mismatches 54; Indels 9; Gaps 4;

QY 11 LVISASATHEAEQNDVSVPKRSVAQAQNSAEVVRCLNSALOVGCGAPACLENSTCDTGM 70

DB 12 LVLTATATFDPEA-SPRRARFSSNSPSDVACLNGALAVGCGTFALENSTCDTGM 70

QY 71 YDICKSFLYSAAKFDTOGKAFFVKESLKCIAANGVTSKVFLAIRRCSTFORMIAEVEECYS 130

DB 71 HDICQLPFHTAATNTQGTFTVKESLRCIAANGVTSKVFTTIRRCGVFORMISEVEECYS 130

QY 131 KLVCSIAKRNPEAITEVWQLPNHPSNRYNRLVRSLLCEDEDTVSTTRDSLMEXIGNM 190

DB 131 RLDCIGVARSNPEAIGEVVQVPAHFPNRYYSTLLQSLACDEETVAVVRAGLVARLGPD 190

QY 191 ASLPHILQTDHCAOTHPADFN-----RRRTNEPQKLVLLNLRGEEDSPSHI 239

DB 191 ETLFQLQLQKHCPOGNSAPAGWRWPMGSPSPFKI-QPSMRGRD--PTHLL 241

RESULT 12

AA55749

ID AAY55749 standard; Protein; 170 AA.

XX AAY55749;

AC AAY55749;

DT 11-FEB-2000 (first entry)

XX A. australis stanniocalcin polypeptide.

XX Stanniocalcin-alpha polypeptide; teleocalcin; hypocalcin; hypercalcemic;

KW anti-hypercalcemic glycoprotein hormone; corpuscles of stannius; PTH;

KW parathyroid hormone; bone reabsorption; osteoporosis; gene therapy; bone;

KW electrolyte disorder; renal; heart disease; osteopetrosis; human;

KW Paget's disease; hypercalcemia.

XX Anguilla australis.

OS US5994103-A.

PN 30-NOV-1999.

PD 02-JUN-1995; 95US-0460529.

PF 10-NOV-1994; 94WO-US13206.

PR (HUMA-) HUMAN GENOME SCI INC.

XX Fleischmann RD, Olsen HS;

XX WPI; 2000-038260/03.

XX Isolated nucleic acids encoding human stanniocalcin-alpha useful for

PT treating electrolyte disorders which lead to renal, bone and heart

PT diseases, osteoporosis and Paget's disease -

PS Disclosure; Fig 2; 21pp; English.

XX The invention provides a human stanniocalcin-alpha polypeptide (also

CC called teleocalcin and hypocalcin). Stanniocalcin-alpha is an anti-

CC hypercalcemic glycoprotein hormone produced by the corpuscles of

CC stannius. It has a similar reported biological activity to that of

CC parathyroid hormone (PTH) and both these proteins exhibit dual functions

CC in mammals. They exert hypercalcemic activity due to stimulation of bone

CC reabsorption. Further PTH has a biphasic action on bone metabolism (i.e.

CC at low doses it increases bone formation and at high doses it increases

CC bone reabsorption). Accordingly, human stanniocalcin-alpha and antagonists

CC of it (under different circumstances) may be used to treat osteoporosis.

CC The DNA may be used to produce human stanniocalcin-alpha according to

CC standard recombinant DNA methodologies. The human stanniocalcin-alpha may

CC be produced either in vitro in a fermentation culture or in vivo as part

CC of a gene therapy protocol, and may be used to treat electrolyte

disorders which lead to renal, bone and heart diseases. Due to the biphasic nature of stanniocalcin-alpha it may be used to treat osteoporosis, osteopetrosis and Paget's disease. Alternatively, the polypeptides may be used as antigens in the production of antibodies to stanniocalcin-alpha and to assay for agonists and antagonists of its activity. The antibodies and antagonists may be used to inhibit the activity of stanniocalcin-alpha and may be used to treat osteoporosis and hypercalcaemia. The present sequence represents a stanniocalcin from Anguilla australis.

Query Match 49.5%; Score 628; DB 21; Length 170;
Best Local Similarity 66.5%; Pred. No. 2,4e-57;
Matches 113; Conservative 30; Mismatches 27; Indels 0; Gaps 0;
QY 28 SPRKSRVAQNSAEVVRCLNSALQVCGGAFACLENSTCDTDGMYDICKSFLYSAAKFDQ 87
DB 1 SPRTARFSASSPDSVARCLNGALQVCGSAFACLDNSTCNTDGMHICRSFLHGAAKFDQ 60
QY 88 GKAFVKESLKCANGVTSKVFLAIRRCSTFORMIAEVOECYKLVNCSIAKRNPPEALTE 147
DB 61 GKTFFVKESLKCANGVTSKVFLAIRRCSTFORMIAEVOECYKLVNCSIAKRNPPEALTE 147
QY 148 VVQLPNHFSNRYNRLVRSLLCEDTSTVIRDSLMKIGPNMASLPHIL 197
DB 121 VAQVPSQPPNRYSTLLQSLTCDTVEQVRAGLVRSLRLEPMGVLFQLL 170

RESULT 13
ABB31928
ID ABB31928 standard; Peptide; 70 AA.
AC ABB31928;
XX
DT 01-FEB-2002 (first entry)
XX
DE Peptide #4579 encoded by breast cell single exon nucleic acid probe.
KW Human; microarray; single exon probe; gene expression; breast;
KW disease; cancer.
XX
OS Homo sapiens.
XX
PN WO200157271-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00662.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
WPI; 2001-496933/54.
XX
DR New spatially-addressable set of single exon nucleic acid probes,
PT useful for measuring gene expression in sample derived from human
PT breast, comprises number of single exon nucleic acid probes -
XX
XX
PS Claim 27; SEQ ID NO 14896; 327pp + sequence listing; English.
XX
XX The invention relates to a spatially-addressable set of single exon
CC nucleic acid probes for measuring gene expression in a sample derived
CC from human breast and BT 474 cells. The method involves contacting

the probes with a collection of detectably labelled nucleic acids derived from mRNA of human breast, and then measuring the label bound to each probe of the microarray. The probes are useful for verifying the expression of regions of genomic DNA predicted to encode proteins. They are useful for gene discovery, and for determining predisposition and/or prognosing breast disease. Gene expression analysis is useful for assessing the toxicity of chemical agents on cells. The microarray of this invention presents a far greater diversity of probes for measuring gene expression, with far less bias than expressed sequence tag microarrays. The method is suitable for rapid production of functional information from genomic sequence. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention.
CC Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Query Match 28.2%; Score 358; DB 22; Length 70;
Best Local Similarity 100.0%; Pred. No. 1.1e-29;
Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 88 GKAFVKESLKCANGVTSKVFLAIRRCSTFORMIAEVOECYKLVNCSIAKRNPPEALTE 147
DB 1 GKAFVKESLKCANGVTSKVFLAIRRCSTFORMIAEVOECYKLVNCSIAKRNPPEALTE 60
QY 148 VVQLPNHFSN 157
DB 61 VVQLPNHFSN 70

RESULT 14
ABB37166
ID ABB37166 standard; Peptide; 70 AA.
XX
AC ABB37166;
XX
DT 04-FEB-2002 (first entry)
XX
DE Peptide #4672 encoded by human foetal liver single exon probe.
KW Human; foetal liver; gene expression; single exon nucleic acid probe.
XX
OS Homo sapiens.
XX
PN WO200157277-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00669.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
WPI; 2001-483447/52.
XX
DR Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human fetal liver -
PT
XX
PS Claim 27; SEQ ID NO 29801; 639pp + sequence listing; English.
XX
XX The invention relates to a single exon nucleic acid probe for
CC measuring human gene expression in a sample derived from human foetal

CC liver. The single exon nucleic acid probes may be used for predicting,
CC measuring and displaying gene expression in samples derived from human
CC fecal liver. The present sequence is a peptide encoded by a single exon
CC nucleic acid probe of the invention.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at [ftp.wipo.int/pub/published pct sequences](http://ftp.wipo.int/pub/published/pct/sequences).

CC Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the patent office.

CC	from WIPO at ftp.v
XX	
SQ	Sequence 70 AA;

Query Match 28.2%; Score 358; DB 22; Length 70;
Best Local Similarity 100.0%; Pred. No. 1.1e-29;
Matches 70; Conservative 0; Mismatches 0; Indels

Qy	88 GKAFVKESLKCIANGVTSKVFLAIRRCSTFORMIAEVQEECYSKLNVCISIAKRNPRAITE	147
Dd	1 GKAFVKESLKCIANGVTSKVFLAIRRCSTFORMIAEVQEECYSKLNVCISIAKRNPRAITE	60

Db 1 G K A F V K E S L K C I A N G V T S K V F L A I R R C S T F Q R M I A E V Q E E C Y S K L N V C S I A K R N P E A I T E 60

Qy 148 VVOLPNHFSN 157

Db 61 WVLPNHESN 70

RESULT 15

ABB22472

ID ABB22472 standard; Protein: 70 AA.

AC ABB22472:

DT 23-JAN-2002 (first entry)

Protein #4471 encoded by probe for measuring heart cell gene expression.

Human; gene expression; heart; microarray; vascular system;
cardiovascular disease; hypertension; cardiac arrhythmia;
congenital heart disease.

OS Homo sapiens.

XX
PN
WO200157274-A2.

09-AUG-2001.

30-JAN-2001: 2001WO-US00666.

PR 04-FEB-2000; 2000US-0180312.

PR 26-MAY-2000; 2000US-0207456.

PR 30-JUN-2000; 2000US-0608408.

PR 03-AUG-2000; 2000US-0632366.

PR 21-SEP-2000; 2000US-0234687.

PR 27-SEP-2000; 2000US-0236359.

PR 04-OCT-2000; 2000GB-0024263.
XX

XX PA (MOLE-) MOLECULAR DYNAMICS INC.

PI	Penn SG,	Hanzel DK,	Chen W,	Rank DR:
XX				

DR WPI: 2001-488899/53.

Single exon nucleic acid probes for analyzing gene expression in human hearts.

PS
XX
Claim 15; SEO ID No 24242: 530pp: English.

The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart (see ABA21533-ABA41305). The present sequence is a protein encoded by one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and congenital heart disease.

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OM protein - protein search, using sw model

Run on: June 12, 2003, 19:53:58 ; Search time 35 Seconds
(without alignments)
207.642 Million cell updates/sec

Title: US-09-705-500A-3
Perfect score: 1268
Sequence: 1 MLQNSAVLLVLVISATHE.....NLRGEDSPSHIKRTSHESA 247

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/prodata/2/1aa/5A-COMB.pep.*
2: /cgn2_6/prodata/2/1aa/5B-COMB.pep.*
3: /cgn2_6/prodata/2/1aa/6A-COMB.pep.*
4: /cgn2_6/prodata/2/1aa/6B-COMB.pep.*
5: /cgn2_6/prodata/2/1aa/PCTUS-COMB.pep.*
6: /cgn2_6/prodata/2/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1268	100.0	247	2	US-08-208-005C-2
2	1268	100.0	247	2	US-09-038-597A-2
3	1268	100.0	247	2	US-08-460-529B-10
4	1268	100.0	247	2	US-08-431-117A-2
5	660.5	52.1	204	2	US-08-208-005C-5
6	660.5	52.1	204	2	US-09-038-597A-5
7	628	49.5	170	2	US-08-460-529B-9
8	354.5	28.0	296	3	US-08-831-132-14
9	354.5	28.0	296	4	US-09-416-150-14
10	354	27.9	302	3	US-08-831-132-2
11	354	27.9	302	4	US-09-416-150-2
12	333.5	26.3	251	2	US-08-460-529B-2
13	89.5	7.1	10182	4	US-09-134-001C-3159
14	85.5	6.7	656	4	US-09-134-001C-4322
15	83	6.5	417	4	US-09-134-001C-3810
16	82	6.5	362	4	US-09-134-001C-4670
17	81	6.4	680	4	US-09-298-924-4
18	81	6.4	720	2	US-08-840-236-1
19	81	6.4	720	2	US-08-505-448A-1
20	79.5	6.3	708	1	US-08-145-681-4
21	79.5	6.3	708	1	US-08-453-703-4
22	79.5	6.3	708	2	US-08-456-106-4
23	79.5	6.3	708	3	US-08-456-108-4
24	79.5	6.3	708	4	US-09-265-577-4
25	78	6.2	315	4	US-09-184-964-4
26	77.5	6.1	467	2	US-08-686-599A-17
27	76.5	6.0	315	4	US-09-615-192A-378

28	76	6.0	2802	4	US-09-542-331-1	Sequence 1, Appli
29	76	6.0	2802	4	US-09-510-791-1	Sequence 1, Appli
30	75.5	6.0	452	2	US-08-686-599A-18	Sequence 18, Appli
31	75.5	6.0	493	2	US-08-686-599A-5	Sequence 5, Appli
32	75.5	6.0	493	2	US-08-686-599A-16	Sequence 16, Appli
33	75.5	6.0	733	3	US-08-725-459B-29	Sequence 29, Appli
34	75	5.9	1257	4	US-09-220-641-3	Sequence 3, Appli
35	74.5	5.9	3696	4	US-09-134-001C-5080	Sequence 5080, Ap
36	74.5	5.9	323	6	5185254-4	Patent No. 5185254
37	74.5	5.9	533	2	US-08-770-544-4	Sequence 4, Appli
38	74	5.8	341	4	US-09-134-001C-4268	Sequence 4268, Ap
39	73.5	5.8	861	1	US-08-484-105-18	Sequence 18, Appli
40	73.5	5.8	861	1	US-08-484-106-18	Sequence 18, Appli
41	73.5	5.8	920	1	US-08-451-715A-2	Sequence 2, Appli
42	73	5.8	511	3	US-09-105-039A-2	Sequence 2, Appli
43	73	5.8	530	3	US-09-105-039A-4	Sequence 4, Appli
44	73	5.8	1093	5	PCT-US93-03077-1	Sequence 1, Appli
45	72.5	5.7	334	1	US-08-287-442-9	Sequence 9, Appli

ALIGNMENTS

RESULT 1
US-08-208-005C-2
; Sequence 2, Application US/08208005C
; Patent No. 5837498
; GENERAL INFORMATION:
; APPLICANT: OLSEN, ET AL.
; TITLE OF INVENTION: Corpuscles of Stannius Protein, Stanniocalcin
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/208,005C
; FILING DATE: 8 MARCH 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: FERRARO, GREGORY D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-78
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 247 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
; US-08-208-005C-2

Query Match 100.0%; Score 1268; DB 2; Length 247;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLQNSAVLLVLVISATHEAQNDSPSRVAAQNSAEVVRCLNSALQVCGCAFL 60
|||||

Db 1 MLQNSAVLLVLVISASATHEAEQNDVSVPKSRVAAQNSAEVVRCLNSALQVCGCAFACL 60
QY 61 ENSTCDTDMYDICKSFYLSAAKFDTOGKAFVKESLKCICANGVTSKVFLAIRRCSTFORM 120
Db 61 ENSTCDTDMYDICKSFYLSAAKFDTOGKAFVKESLKCICANGVTSKVFLAIRRCSTFORM 120
QY 121 IAEVQEECYSKLVNCSIAKRNPPEAITEVVQLPNHFSNRYNRLVRSLLCEDDTVSTIRD 180
Db 121 IAEVQEECYSKLVNCSIAKRNPPEAITEVVQLPNHFSNRYNRLVRSLLCEDDTVSTIRD 180
QY 181 SLMEKIGPNMASLPHILOTHDCAQTHPRADFNRRRTNEPQKLKVLRLNRGEEDESPSHIK 240
Db 181 SLMEKIGPNMASLPHILOTHDCAQTHPRADFNRRRTNEPQKLKVLRLNRGEEDESPSHIK 240
QY 241 RTSHESA 247
Db 241 RTSHESA 247

RESULT 2

US-09-038-597A-2
; Sequence 2, Application US/09038597A
; Patent No. 5877290
; GENERAL INFORMATION:
; APPLICANT: OLSEN, ET AL.
; TITLE OF INVENTION: Capsules of Stannius Protein,
; CORRESPONDENCE ADDRESS:
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/038,597A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/208,005
; FILING DATE: 8-MARCH-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: FERRARO, GREGORY D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-78
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 247 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
US-09-038-597A-2

Query Match 100.0%; Score 1268; DB 2; Length 247;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLQNSAVLLVLVISASATHEAEQNDVSVPKSRVAAQNSAEVVRCLNSALQVCGCAFACL 60
Db 1 MLQNSAVLLVLVISASATHEAEQNDVSVPKSRVAAQNSAEVVRCLNSALQVCGCAFACL 60
QY 61 ENSTCDTDMYDICKSFYLSAAKFDTOGKAFVKESLKCICANGVTSKVFLAIRRCSTFORM 120

Db 61 ENSTCDTDMYDICKSFYLSAAKFDTOGKAFVKESLKCICANGVTSKVFLAIRRCSTFORM 120
QY 121 IAEVQEECYSKLVNCSIAKRNPPEAITEVVQLPNHFSNRYNRLVRSLLCEDDTVSTIRD 180
Db 121 IAEVQEECYSKLVNCSIAKRNPPEAITEVVQLPNHFSNRYNRLVRSLLCEDDTVSTIRD 180
QY 181 SLMEKIGPNMASLPHILOTHDCAQTHPRADFNRRRTNEPQKLKVLRLNRGEEDESPSHIK 240
Db 181 SLMEKIGPNMASLPHILOTHDCAQTHPRADFNRRRTNEPQKLKVLRLNRGEEDESPSHIK 240
QY 241 RTSHESA 247
Db 241 RTSHESA 247

RESULT 3

US-08-460-529B-10
; Sequence 10, Application US/08460529B
; Patent No. 5994103
; GENERAL INFORMATION:
; APPLICANT: OLSEN, ET AL.
; TITLE OF INVENTION: Human Stanniocalcin-alpha
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,529B
; FILING DATE: June 2, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/13206
; FILING DATE: 10 NOV 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-334 (PFI43)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 247 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
US-08-460-529B-10

Query Match 100.0%; Score 1268; DB 2; Length 247;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLQNSAVLLVLVISASATHEAEQNDVSVPKSRVAAQNSAEVVRCLNSALQVCGCAFACL 60
Db 1 MLQNSAVLLVLVISASATHEAEQNDVSVPKSRVAAQNSAEVVRCLNSALQVCGCAFACL 60
QY 61 ENSTCDTDMYDICKSFYLSAAKFDTOGKAFVKESLKCICANGVTSKVFLAIRRCSTFORM 120
Db 61 ENSTCDTDMYDICKSFYLSAAKFDTOGKAFVKESLKCICANGVTSKVFLAIRRCSTFORM 120
QY 121 IAEVQEECYSKLVNCSIAKRNPPEAITEVVQLPNHFSNRYNRLVRSLLCEDDTVSTIRD 180

Db 121 IAEVQEECYKUNVCSIAKRNPEAITEVVQLPNHFSNRYNRLVRSLLCEDEDTVSTIRD 180
QY 181 SLMEKIGPNMASLPHILOTHCAQTHPRADFNRRRTNEPQKLKVLRLNLRGEEDSPSHIK 240
Db 181 SLMEKIGPNMASLPHILOTHCAQTHPRADFNRRRTNEPQKLKVLRLNLRGEEDSPSHIK 240
QY 241 RTSHEA 247
Db 241 RTSHEA 247

RESULT 4

US-08-431-117A-2
; Sequence 2, Application US/08431117A
; Patent No. 5994301
; GENERAL INFORMATION:
; APPLICANT: OLSEN, ET AL.
; TITLE OF INVENTION: Corpuscles of Stannius Protein, Stanniocalcin
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/431,117A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/208,005
; FILING DATE: 8 MARCH 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: FERRARO, GREGORY D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-296
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 247 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
US-08-431-117A-2

Query Match 100.0%; Score 1268; DB 2; Length 247;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLQNSAVLLVLVISASATHEAEQNDVSVPKRSRVAQAQNSAEVVRCLNSALQVCGGAPACL 60
Db 1 MLQNSAVLLVLVISASATHEAEQNDVSVPKRSRVAQAQNSAEVVRCLNSALQVCGGAPACL 60
QY 61 ENSTCDTGMVDICKSFLYSAAKPTQKAFVKESLKCIAANGVTSKVFLAIRRSTFORM 120
Db 61 ENSTCDTGMVDICKSFLYSAAKPTQKAFVKESLKCIAANGVTSKVFLAIRRSTFORM 120
QY 121 IAEVQEECYKUNVCSIAKRNPEAITEVVQLPNHFSNRYNRLVRSLLCEDEDTVSTIRD 180
Db 121 IAEVQEECYKUNVCSIAKRNPEAITEVVQLPNHFSNRYNRLVRSLLCEDEDTVSTIRD 180
QY 181 SLMEKIGPNMASLPHILOTHCAQTHPRADFNRRRTNEPQKLKVLRLNLRGEEDSPSHIK 240

Db 181 SLMEKIGPNMASLPHILOTHCAQTHPRADFNRRRTNEPQKLKVLRLNLRGEEDSPSHIK 240
QY 241 RTSHEA 247
Db 241 RTSHEA 247

RESULT 5

US-08-208-005C-5
; Sequence 5, Application US/08208005C
; Patent No. 5837498
; GENERAL INFORMATION:
; APPLICANT: OLSEN, ET AL.
; TITLE OF INVENTION: Corpuscles of Stannius Protein, Stanniocalcin
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/208,005C
; FILING DATE: 8 MARCH 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: FERRARO, GREGORY D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-78
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 204 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
US-08-208-005C-5

Query Match 52.1%; Score 660.5; DB 2; Length 204;
Best Local Similarity 60.8%; Pred. No. 2.4e-67;
Matches 118; Conservative 38; Mismatches 37; Indels 1; Gaps 1;
QY 11 LVISASATHEAEQNDVSVPKRSRVAQAQNSAEVVRCLNSALQVCGGAPACLENSTCDTGM 70
Db 12 LVLGTATFTDDPEA-SPRRARFSSNSPSDVARCLNGALVCGGTACLENSTCDTGM 70
QY 71 YDICKSFLYSAAKPTQKAFVKESLKCIAANGVTSKVFLAIRRSTFORMIAEVOEECY 130
Db 71 HDICQLFFHTAATNTQKTFVKESLKCIAANGVTSKVFLAIRRSTFORMIAEVOEECY 130
QY 131 KLVNCSIAKRNPEAITEVVQLPNHFSNRYNRLVRSLLCEDEDTVSTIRDSLMKIGPNM 190
Db 131 RLDICGVARSNPEAIGEVQVQFAHPFPNRYSTLLQLSLACDEETVAVVRAGLVARLGDM 190
QY 191 ASLPHILOTHCAQ 204
Db 191 ETLFOLLQNHCPQ 204

RESULT 6
US-09-038-597A-5
; Sequence 5, Application US/09038597A
; Patent No. 5877290
; GENERAL INFORMATION:
; APPLICANT: OLSEN, ET AL.
; TITLE OF INVENTION: Corpuscles of Stannius Protein,
; TITLE OF INVENTION: Stanniocalcin
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/038,597A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/208,005
; FILING DATE: 8-MARCH-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: FERRARO, GREGORY D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-78
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 204 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
US-09-038-597A-5

Query Match 52.1%; Score 660.5; DB 2; Length 204;
Best Local Similarity 60.8%; Pred. No. 2.4e-67;
Matches 118; Conservative 38; Mismatches 37; Indels 1; Gaps 1;
QY 11 LVISATHEAEQNDVSPPKSRVAAQNSAEVVRCLNSALQVCGGAFACLENSTCDTDM 70
Db 12 LVLGTAATFDTPEEA-SPRRARFSSNSPSDVARCLNGALVCGGTACLENSTCDTDM 70
QY 71 YDICKSFLYSAAKFTQGHAFKVESLKCIANGVTSKVFLAIRRCSTFORMIAEVOECYS 130
Db 71 HDICOLFHTAATFNTQGTFTFKESLRCIANGVTSKVFLAIRRCSTFORMIAEVOECYS 130
QY 131 KLVNCSIAKRNPEATEVVLPHNSRYNRLVRSLLCEDEDVTSTIRDSLMEXIGPNM 190
Db 131 RLIDICGVARSNPEATGEVQVPAHPNRYSTLQSLACDEBTAVVRAGLVRLGPDM 190
QY 191 ASLPHILOTDHCAQ 204
Db 191 ETLFOLLQNKHCPO 204

RESULT 7
US-08-460-529B-9
; Sequence 9, Application US/08460529B
; Patent No. 5954103
; GENERAL INFORMATION:
; APPLICANT: OLSEN, ET AL.
; TITLE OF INVENTION: Human Stanniocalcin-alpha

; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,529B
; FILING DATE: June 2, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/13206
; FILING DATE: 10 NOV 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-334 (PFI43)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 170 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
US-08-460-529B-9

Query Match 49.5%; Score 628; DB 2; Length 170;
Best Local Similarity 66.5%; Pred. No. 9.5e-64;
Matches 113; Conservative 30; Mismatches 27; Indels 0; Gaps 0;
QY 28 SPRKSRVAAQNSAEVVRCLNSALQVCGGAFACLENSTCDTDMYDICKSFLYSAAKFTQ 87
Db 1 SPRTARFSASSPSDVARCLNGALQVCGSAPACLDNSTCNTDGMHEICRSFLHGAAKFTQ 60
QY 88 GKAFKESLKCIANGVTSKVFLAIRRCSTFORMIAEVOECYSKLVNCSIAKRNPEATE 147
Db 61 GKTFRKESLKCIANGVTSKVFLAIRRCSTFORMIAEVOECYSKLVNCSIAKRNPEAME 120
QY 148 VVQLPHNSRYNRLVRSLLCEDEDVTSTIRDSLMEXIGPNMASLPHIL 197
Db 121 VAQVPSQFPNRYSTLLQSLTCDDETVQVRAGLVSRLEPEMGVLFOLL 170

RESULT 8
US-08-831-132-14
; Sequence 14, Application US/08831132
; Patent No. 6008322
; GENERAL INFORMATION:
; APPLICANT: Kuestner, Rolf E.
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Lok, Si
; APPLICANT: Biddle, Michele
; APPLICANT: Downey, William
; TITLE OF INVENTION: STANNIOCALCIN-2
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/831,132
FILING DATE: US/08/831,132

CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Sawislak, Deborah A.
REGISTRATION NUMBER: 37,438
REFERENCE/DOCKET NUMBER: 96-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6672
TELEFAX: 206-442-6678
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 296 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-831-132-14

Query Match 28.0%; Score 354.5; DB 3; Length 296;
Best Local Similarity 31.7%; Pred. No. 3.6e-32;
Matches 85; Conservative 45; Mismatches 109; Indels 29; Gaps 5;

QY 7 VLLVLVISASATHEAQNDSVSP-----RKSrvAAQNSAEVVRCLNSALQVCGGA 56
DB 10 VTLALVF--ATLDPAGQTDSTNPPGPDQRSSQKGRSLQNTAEIQHCLVNAGDVGGCV 67
QY 57 FACLENSTCDTGMVDICKSFLYSAAKFDTOGKAFVKESLKCANGVTSKVLAIKRCST 116
DB 68 FECFENNACEIQGLHGICWTFLHNAGKFDAGKSPFKDALRCKAHALRHKFGCISRKCPA 127
QY 117 FORMIAEQVECYKLVNCSIAKRNPEAITEVQVLPNHFNSRYNRLVRSLLCEDTIVS 176
DB 128 IREVMFQIQRECYLKHDLCSAAQENVGIVEMIHFKDLLLHPEYVDLVNLLTGGEDVKE 187
QY 177 TIROSLMEKIGPNMASLPHIL-----OTDHCQAOTH-----PRADFNRRTNEPQKLKV 224
DB 188 AVTSSVQAQCSQSGGLCSILSFCTSNIQRPPTAAPEHQPLADRAQLSRPHRRDTHHLT 247
QY 225 LLRNLGRGEEDSPSHIK-----RTSHESA 247
DB 248 ANRGAKGERGSKSHNAHARGTGGQSA 275

RESULT 9
US-09-416-150-14
Sequence 14, Application US/09416150
Patent No. 6171822
GENERAL INFORMATION:
APPLICANT: Kuestner, Rolf E.
Konklin, Darrell C.
Lok, Si
Buddle, Michele
Downey, William
TITLE OF INVENTION: STANNIOCALCIN-2
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/416,150
FILING DATE: 11-Oct-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/831,132
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Sawislak, Deborah A.
REGISTRATION NUMBER: 37,438
REFERENCE/DOCKET NUMBER: 96-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6672
TELEFAX: 206-442-6678
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 296 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-416-150-14

Query Match 28.0%; Score 354.5; DB 4; Length 296;
Best Local Similarity 31.7%; Pred. No. 3.6e-32;
Matches 85; Conservative 45; Mismatches 109; Indels 29; Gaps 5;
QY 7 VLLVLVISASATHEAQNDSVSP-----RKSrvAAQNSAEVVRCLNSALQVCGGA 56
DB 10 VTLALVF--ATLDPAGQTDSTNPPGPDQRSSQKGRSLQNTAEIQHCLVNAGDVGGCV 67
QY 57 FACLENSTCDTGMVDICKSFLYSAAKFDTOGKAFVKESLKCANGVTSKVLAIKRCST 116
DB 68 FECFENNACEIQGLHGICWTFLHNAGKFDAGKSPFKDALRCKAHALRHKFGCISRKCPA 127
QY 117 FORMIAEQVECYKLVNCSIAKRNPEAITEVQVLPNHFNSRYNRLVRSLLCEDTIVS 176
DB 128 IREVMFQIQRECYLKHDLCSAAQENVGIVEMIHFKDLLLHPEYVDLVNLLTGGEDVKE 187
QY 177 TIROSLMEKIGPNMASLPHIL-----OTDHCQAOTH-----PRADFNRRTNEPQKLKV 224
DB 188 AVTSSVQAQCSQSGGLCSILSFCTSNIQRPPTAAPEHQPLADRAQLSRPHRRDTHHLT 247
QY 225 LLRNLGRGEEDSPSHIK-----RTSHESA 247
DB 248 ANRGAKGERGSKSHNAHARGTGGQSA 275

RESULT 10
US-08-831-132-2
Sequence 2, Application US/08831132
Patent No. 6008322
GENERAL INFORMATION:
APPLICANT: Kuestner, Rolf E.
Konklin, Darrell C.
Lok, Si
Buddle, Michele
Downey, William
TITLE OF INVENTION: STANNIOCALCIN-2
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/08/831,132
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A.
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 96-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6672
; TELEFAX: 206-442-6678
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 302 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-831-132-2

Query Match      27.9%; Score 354; DB 3; Length 302;
Best Local Similarity 32.4%; Pred. No. 4.2e-32;
Matches 83; Conservative 45; Mismatches 102; Indels 26; Gaps 4;

QY 9 LVLVIS-----ASATHEAE-QNDSVSPKRSRVAQNSAEVVRCLNSALQVCGCAFCL 60
DB 12 LALVLATFDPARGTDATNPPEGPQDRSSQKGRSLQNTAEIQHCLVNAGDVCGVFECE 71
QY 61 ENSTCDTGMVDICKSFLYSAKFTDCKAFVKESLKCIAANGVTSKVFLAIRRCSTFORM 120
DB 72 ENNCEIRGLHGICMTFLHNAGKFDQKSFIDKALKCAHALRHFCCISRKCPAIREM 131
QY 121 IAEVQECYSKLVNCSIAKRNPEATEVVLQPNHFSNRYNRLVRSLLCEDEDTVSTIRD 180
DB 132 VSQLORECYLKHDLCAAAQENTRVIVEMHFKDILLHPEYVDVLLNLLTTCGEEVKEATH 191
QY 181 SMEKIGPNMASLPHILO-TDCAQTHPRADNRRRTNEPKL----- 222
DB 192 SVQVQCEQNWGSLCSILSFCTSAIQKPTAPPERPQVDRTKLSRAHNGEAGHHLPEPSS 251
QY 223 KVLRLNLRGEEDSPSH 238
DB 252 RETGRGAKGERGSKSH 267

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RESULT 11
US-09-416-150-2
; Sequence 2, Application US/09416150
; Patent No. 6171822
; GENERAL INFORMATION:
; APPLICANT: Kuestner, Rolf E.
; Lok, Si
; Biddle, Michele
; Downey, William
; TITLE OF INVENTION: STANNIOCALCIN-2
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/416,150
; FILING DATE: 11-Oct-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/831,132

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; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A.
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 96-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6672
; TELEFAX: 206-442-6678
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 302 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
; US-09-416-150-2

Query Match      27.9%; Score 354; DB 4; Length 302;
Best Local Similarity 32.4%; Pred. No. 4.2e-32;
Matches 83; Conservative 45; Mismatches 102; Indels 26; Gaps 4;

QY 9 LVLVIS-----ASATHEAE-QNDSVSPKRSRVAQNSAEVVRCLNSALQVCGCAFCL 60
DB 12 LALVLATFDPARGTDATNPPEGPQDRSSQKGRSLQNTAEIQHCLVNAGDVCGVFECE 71
QY 61 ENSTCDTGMVDICKSFLYSAKFTDCKAFVKESLKCIAANGVTSKVFLAIRRCSTFORM 120
DB 72 ENNCEIRGLHGICMTFLHNAGKFDQKSFIDKALKCAHALRHFCCISRKCPAIREM 131
QY 121 IAEVQECYSKLVNCSIAKRNPEATEVVLQPNHFSNRYNRLVRSLLCEDEDTVSTIRD 180
DB 132 VSQLORECYLKHDLCAAAQENTRVIVEMHFKDILLHPEYVDVLLNLLTTCGEEVKEATH 191
QY 181 SMEKIGPNMASLPHILO-TDCAQTHPRADNRRRTNEPKL----- 222
DB 192 SVQVQCEQNWGSLCSILSFCTSAIQKPTAPPERPQVDRTKLSRAHNGEAGHHLPEPSS 251
QY 223 KVLRLNLRGEEDSPSH 238
DB 252 RETGRGAKGERGSKSH 267

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RESULT 12
US-08-460-529B-2
; Sequence 2, Application US/08460529B
; Patent No. 5994103
; GENERAL INFORMATION:
; APPLICANT: OLSEN, ET AL.
; TITLE OF INVENTION: Human Stanniocalcin-alpha
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,529B
; FILING DATE: June 2, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/13206
; FILING DATE: 10 NOV 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073

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; REFERENCE/DOCKET NUMBER: 325800-334 (PF143).
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
US-08-460-529B-2
; Query Match 26.3%; Score 333.5; DB 2; Length 251;
; Best Local Similarity 32.6%; Pred. No. 6.9e-30;
; Matches 78; Conservative 43; Mismatches 89; Indels 29; Gaps 5;

QY 9 LVLVIS-----ASATHEAE-QNDSVSPKSRVAQAQNSAEVVRCLNSALQVGGGAPACL 60
Db 12 LALVLATDPARGTDATPPGPGQDRSSQOQGRSLQNTAEIQHCLVNAGDVGGCGVFCF 71

QY 61 ENSTCDTDMYDICKSFYLSAAKFTQGFVKESELKCIANGVTSKVFALAIRRCSTFORM 120
Db 72 ENNSCEIRGLHCICMTFLNACKGPDQKSFIDKALKCAHALRHRFCISRKCPAIREM 131

QY 121 IAEVQEECYSLNVCISIAKRNPFAITEVVLQPNHFSNRYNRLVRSLLCEDEDTVSTIRD 180
Db 132 VSQLRGCTGLKHLCAAQAGTRVIMTHFKDLLLHGYPVDLVNLLTTCGEEVKEAITH 191

QY 181 SLMEKIGPMASLPHILOTHCAQ-----THP-----RADFNRRRTNEQ 220
Db 192 SVQVCEQNWGSLCSIL--SFCTSDIQKPTAPPERPQVDRTKLSRAHGHGRTSPPR 248

RESULT 13
US-09-134-001C-3159
; Sequence 3159, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 3159
; LENGTH: 10182
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3159

Query Match 7.1%; Score 89.5; DB 4; Length 10182;
Best Local Similarity 22.0%; Pred. No. 13;
Matches 50; Conservative 38; Mismatches 78; Indels 61; Gaps 11;

QY 17 ATHEAEQ---NDSVSPKSRVA-----AQAQNSAEVVRCLNSALQ 51
Db 2954 AKNEAERILGND--NPQVSQVTOALNKIKAIQPKLTAENMLQNKENTLVNAKRN--- 3008

QY 52 VCCGAFACLENSTCDTDMYDICKSFL--YSNAKFTQGFVKESELKCIANG----- 102
Db 3009 -----LENAVNDTDPHTGTOETINYNNAKKEAQAQNE--IQKANMIINNGDATAQDI 3058

QY 103 -----VTSKVFALAIRRCSTFORMIAEVEECYSLK--NVCSIAKRNPFAITEVVLQPNHF 155
Db 3059 SSEKSKVEQVQLQNAKNDLRAKRELOQTAYNKLIQNVNTGKK-PSSIQNYKSARNI 3117

QY 156 SNRY--YNRLVRSLLCEDEDTVSTIRDSL--MEKIGPMASLPHILQ 198

; REFERENCE/DOCKET NUMBER: 3118 ENQYNTAKNEAHNVLENTPTVNAVEDALRKINAIOQEVTKAINILQ 3164
; Sequence 4322, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 4322
; LENGTH: 656
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4322

Query Match 6.7%; Score 85.5; DB 4; Length 656;
Best Local Similarity 25.6%; Pred. No. 0.6;
Matches 42; Conservative 21; Mismatches 70; Indels 31; Gaps 6;

QY 35 AQAQNSAEVVRCLNSALQVGGGAPACLENSTCDTDMY-----DICK 75
Db 25 SAEKLATEIINLESILELPKGT---BHFVSDLHGEYESFOHVLNRGSGNVRKINDIFK 80

QY 76 SFLYSAAKFTQGFV--KESLKIANGVTSKVFALAIRRCSTFORMIAEVEECYSLNVL 134
Db 81 DKLSQEQEINDLAALVYYPPEEKLKLVKNNFDSIGTLNIWYITIQRLI--DLITYCSSKYTR 139

QY 135 CSIAKRNP-----AITEVVLQPNHFSNR--YYNRLVRSLLCEDE 172
Db 140 SKLRKALPEQVYVYIEELLYKSNFHNKPKPYETLVNQIIELEQ 183

RESULT 15
US-09-134-001C-3810
; Sequence 3810, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 3810
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3810

Query Match 6.5%; Score 83; DB 4; Length 417;
Best Local Similarity 22.6%; Pred. No. 0.58;
Matches 44; Conservative 32; Mismatches 57; Indels 62; Gaps 11;

QY 57 FACLENSTCDT-----GMVDICKSFYLSAAKFTQGFVKESELKCIANGVTSKVFAL 111
Db 266 FIKFEETIETDHTSKOGLVDVIOFS---KDKVTEGKSFYRLNVR-----INSEDIAP 317
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OM protein - protein search, using sw model

Run on: June 12, 2003, 19:56:59 ; Search time 55 Seconds
(without alignments)
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Title: US-09-705-500A-3
Perfect score: 1268
Sequence: 1 MLQNSAVLLVLVISASATHE.....NLRGEDSPSHIKRTSHESA 247

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Gapop 10.0 , Gapext 0.5

Searched: 392085 seqs, 103240269 residues
Total number of hits satisfying chosen parameters: 392085

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*
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3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pdb.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pdb.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pdb.*
6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pdb.*
7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pdb.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pdb.*
9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pdb.*
10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pdb.*
11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pdb.*
12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pdb.*
13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pdb.*
14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pdb.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1268	100.0	247	10	US-09-840-989A-2
2	1268	100.0	247	10	US-09-361-736-10
3	1268	100.0	247	12	US-10-116-051-2
4	937	73.9	276	10	US-09-925-300-1426
5	662.5	52.2	256	10	US-09-840-989A-3
6	660.5	52.1	204	12	US-10-116-051-10
7	628	49.5	170	10	US-09-361-736-9
8	358	28.3	70	10	US-09-864-761-37770
9	333.5	26.3	251	10	US-09-361-736-2
10	303	23.9	118	12	US-10-116-051-9
11	91	7.2	901	9	US-09-828-062-8
12	81	6.4	720	10	US-09-419-305-1
13	80	6.3	2180	9	US-09-736-968A-110
14	80	6.3	2180	10	US-09-736-969A-96
15	80	6.3	2180	10	US-09-736-960-93
16	78.5	6.2	1288	9	US-09-736-968A-13
17	78.5	6.2	1288	10	US-09-736-969A-13
18	78.5	6.2	1288	10	US-09-736-960-13
19	76	6.0	822	10	US-09-826-312-12

20	76	6.0	1501	10	US-09-924-154-17	Sequence 17, Appl
21	76	6.0	26926	9	US-09-759-508B-2	Sequence 2, Appl
22	75.5	6.0	1338	10	US-09-402-100-4	Sequence 4, Appl
23	75	5.9	454	9	US-09-963-339-2	Sequence 2, Appl
24	75	5.9	1336	9	US-10-278-173-128	Sequence 128, Appl
25	74.5	5.9	211	10	US-09-861-451A-38	Sequence 38, Appl
26	74.5	5.9	323	9	US-10-097-340-314	Sequence 314, Appl
27	74.5	5.9	581	12	US-10-074-527-2	Sequence 2, Appl
28	74.5	5.9	903	9	US-10-087-464-52	Sequence 52, Appl
29	73.5	5.8	301	9	US-09-971-536-55	Sequence 55, Appl
30	73.5	5.8	302	9	US-09-764-868-1069	Sequence 1069, Ap
31	73.5	5.8	302	9	US-09-955-999-94	Sequence 94, Appl
32	73.5	5.8	947	10	US-09-801-574-4	Sequence 4, Appl
33	72.5	5.7	305	9	US-09-764-868-643	Sequence 643, App
34	72.5	5.7	362	10	US-09-815-242-11352	Sequence 11352, A
35	72.5	5.7	1530	9	US-10-118-513A-6	Sequence 6, Appl
36	72.5	5.7	1765	9	US-10-037-182-8	Sequence 8, Appl
37	72.5	5.7	1786	9	US-10-037-182-6	Sequence 6, Appl
38	72.5	5.7	1786	10	US-09-873-676-113	Sequence 113, App
39	72.5	5.7	1786	10	US-09-938-275-6	Sequence 6, Appl
40	72.5	5.7	2266	9	US-10-118-513A-14	Sequence 14, Appl
41	72	5.7	256	9	US-09-925-299-992	Sequence 992, App
42	72	5.7	256	10	US-09-925-299-992	Sequence 992, App
43	72	5.7	583	9	US-10-176-847-64	Sequence 64, Appl
44	71.5	5.6	1481	10	US-09-371-900-40	Sequence 40, Appl
45	71.5	5.6	1481	10	US-09-924-417-60	Sequence 60, Appl

ALIGNMENTS

RESULT 1
US-09-840-989A-2
; Sequence 2, Application US/09840989A
; Patent No. US20020042372A1
; GENERAL INFORMATION:
; APPLICANT: Olsen et al.
; TITLE OF INVENTION: Stanniocalcin Polynucleotides, Polypeptides, and Methods Based The
; FILE REFERENCE: PF108P2
; CURRENT APPLICATION NUMBER: US/09/840,989A
; CURRENT FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: PCT/US00/29432
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,740
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-840-989A-2

Query Match	100.0%	Score	1268	DB	10	Length	247
Best Local Similarity	100.0%	Pred. No.	1.2e-119				
Matches	247	Conservative	0	Mismatches	0	Indels	0
Gaps	0						
Qy	1	MLQNSAVLLVLVISASATHEAQNDVS	PRKSRVAAQNSAEVVRCLNSALQVCGCAFCL	60			
Db	1	MLQNSAVLLVLVISASATHEAQNDVS	PRKSRVAAQNSAEVVRCLNSALQVCGCAFCL	60			
Qy	61	ENSTCDTDGMYDICKSFLYSAAKFTDQ	GKAFVKESLKCIAANGVTSKVFALIRRCSTTF	120			
Db	61	ENSTCDTDGMYDICKSFLYSAAKFTDQ	GKAFVKESLKCIAANGVTSKVFALIRRCSTTF	120			
Qy	121	IAEQVEECYKLVNCSIAKRNPEAITEV	QVLPNFHSRNYNRLVRSLLCEDDTVTTRD	180			
Db	121	IAEQVEECYKLVNCSIAKRNPEAITEV	QVLPNFHSRNYNRLVRSLLCEDDTVTTRD	180			
Qy	181	SLMEKIGPNMASLPHILOTDHCAQTH	PRADPNRRRTNEPQKLKVLRLNRGEEDSPSHIK	240			
Db	181	SLMEKIGPNMASLPHILOTDHCAQTH	PRADPNRRRTNEPQKLKVLRLNRGEEDSPSHIK	240			

QY 241 RTSHESA 247
Db 241 RTSHESA 247

RESULT 2

US-09-361-736-10
; Sequence 10, Application US/09361736
; Patent No. US20020102634A1
; GENERAL INFORMATION:
; APPLICANT: OLSEN, ET AL.
; TITLE OF INVENTION: Human Stannioalcin-alpha
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/361,736
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/460,529
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-334 (PF143)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 247 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
US-09-361-736-10

Query Match 100.0%; Score 1268; DB 10; Length 247;
Best Local Similarity 100.0%; Pred. No. 1.2e-119;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLQNSAVLLVLVISASATHEAEQNDVSVPKSRVAAQNSAEVVRCLNSALQVCGCAFACL 60
Db 1 MLQNSAVLLVLVISASATHEAEQNDVSVPKSRVAAQNSAEVVRCLNSALQVCGCAFACL 60
QY 61 ENSTCDTGMVDICKSFYLSAAKFTDQKAFVKESLKCICANGVTSKVFLAIRRCSTFORM 120
Db 61 ENSTCDTGMVDICKSFYLSAAKFTDQKAFVKESLKCICANGVTSKVFLAIRRCSTFORM 120
QY 121 IAEVQEECYSKLVNCSIAKRNPFAITEVVQLPNHFSNRYNRLVRSLLCEDEDTVSTIRD 180
Db 121 IAEVQEECYSKLVNCSIAKRNPFAITEVVQLPNHFSNRYNRLVRSLLCEDEDTVSTIRD 180
QY 181 SLMEKIGPNMASLPHILOTDHCAQTHPRADFNRRRTNEPQKLKVLRLNRGEEDSPSHIK 240
Db 181 SLMEKIGPNMASLPHILOTDHCAQTHPRADFNRRRTNEPQKLKVLRLNRGEEDSPSHIK 240
QY 241 RTSHESA 247
Db 241 RTSHESA 247

RESULT 3

US-10-116-051-2
; Sequence 2, Application US/10116051
; Patent No. US20020146791A1
; GENERAL INFORMATION:
; APPLICANT: OLSEN et al.
; TITLE OF INVENTION: CORPUSCLES OF STANNIUS PROTEIN, STANNIOALCIN
; FILE REFERENCE: PF108P1D1C1
; CURRENT APPLICATION NUMBER: US/10/116,051
; CURRENT FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 09/312,610
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 08/431,117
; PRIOR FILING DATE: 1995-04-28
; PRIOR APPLICATION NUMBER: 08/208,005
; PRIOR FILING DATE: 1994-03-08
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 2
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-116-051-2

Query Match 100.0%; Score 1268; DB 12; Length 247;
Best Local Similarity 100.0%; Pred. No. 1.2e-119;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLQNSAVLLVLVISASATHEAEQNDVSVPKSRVAAQNSAEVVRCLNSALQVCGCAFACL 60
Db 1 MLQNSAVLLVLVISASATHEAEQNDVSVPKSRVAAQNSAEVVRCLNSALQVCGCAFACL 60
QY 61 ENSTCDTGMVDICKSFYLSAAKFTDQKAFVKESLKCICANGVTSKVFLAIRRCSTFORM 120
Db 61 ENSTCDTGMVDICKSFYLSAAKFTDQKAFVKESLKCICANGVTSKVFLAIRRCSTFORM 120
QY 121 IAEVQEECYSKLVNCSIAKRNPFAITEVVQLPNHFSNRYNRLVRSLLCEDEDTVSTIRD 180
Db 121 IAEVQEECYSKLVNCSIAKRNPFAITEVVQLPNHFSNRYNRLVRSLLCEDEDTVSTIRD 180
QY 181 SLMEKIGPNMASLPHILOTDHCAQTHPRADFNRRRTNEPQKLKVLRLNRGEEDSPSHIK 240
Db 181 SLMEKIGPNMASLPHILOTDHCAQTHPRADFNRRRTNEPQKLKVLRLNRGEEDSPSHIK 240
QY 241 RTSHESA 247
Db 241 RTSHESA 247

RESULT 4

US-09-925-300-1426
; Sequence 1426, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925,300
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: Patent in ver. 2.0
; SEQ ID NO 1426
; LENGTH: 276
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE

LOCATION: (43)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (273)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (275)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-300-1426

Query Match 73.9%; Score 937; DB 10; Length 276;
Best Local Similarity 99.5%; Pred. No. 2.8e-86;
Matches 185; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLQNSAVLLVLVISASATHEAEQNDVSPKRSRVAQAQNSAEVVRCLNSALQVCGGAFACL 60
DB MLQNSAVLLVLVISASATHEAEQNDVSPKRSRVAQAQNSAEVVRCLNSALQVCGGAFACL 148

QY 61 ENSTCDTGMVDICKSFLYSAAKFTQKAFVKESLKCIAANGVTSKVFLAIRRCSTFORM 120
DB ENSTCDTGMVDICKSFLYSAAKFTQKAFVKESLKCIAANGVTSKVFLAIRRCSTFORM 208

QY 121 IAEVOEECYKLVNCSIAKRNPETAEVVLQPNHFSNRYNRLVRSLLCEDEDTVSTIRD 180
DB IAEVOEECYKLVNCSIAKRNPETAEVVLQPNHFSNRYNRLVRSLLCEDEDTVSTIRD 268

QY 181 SLMEKI 186
DB SLMEKI 274

RESULT 5
US-09-840-989A-3
Sequence 3, Application US/09840989A
Patent No. US20020042372A1
GENERAL INFORMATION:
APPLICANT: Olsen et al.
TITLE OF INVENTION: Stanniocalcin Polynucleotides, Polypeptides, and Methods Based Thereon
FILE REFERENCE: PFI08P2
CURRENT APPLICATION NUMBER: US/09/840,989A
CURRENT FILING DATE: 2001-04-25
PRIOR APPLICATION NUMBER: PCT/US00/29432
PRIOR FILING DATE: 2000-10-26
PRIOR APPLICATION NUMBER: US 60/161,740
PRIOR FILING DATE: 1999-10-27
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 256
TYPE: PRT
ORGANISM: Oncorhynchus kisutch
US-09-840-989A-3

Query Match 52.2%; Score 662.5; DB 10; Length 256;
Best Local Similarity 53.4%; Pred. No. 1.1e-58;
Matches 125; Conservative 46; Mismatches 54; Indels 9; Gaps 4;

QY 11 LVISASATHEAEQNDVSPKRSRVAQAQNSAEVVRCLNSALQVCGGAFACLNSTCDTGM 70
DB LVISATATFTDPEEA-SPRRARFSSNSPSDVARCLNGALAVCGGTFACLNSTCDTGM 70

QY 71 YDICKSFLYSAAKFTQKAFVKESLKCIAANGVTSKVFLAIRRCSTFORMIAEVOEECY 130
DB HDICQLFPHTAATNTQKTFVKESLRCIAANGVTSKVFTIRRCGVFQRMISEVOEECY 130

QY 131 KLVNCSIAKRNPETAEVVLQPNHFSNRYNRLVRSLLCEDEDTVSTIRDSLMEXIGPNM 190
DB 131 RLDICGVARSNPEAIGEVVQVPAHFPPNRYSTLLQSLACDEETVAVVRAGLVARLGPDM 190

QY 191 ASLPHILOTDHCAQTHPRADFN-----RRRTNEPKLVLLNLRGEEDSPSHI 239
DB 191 ETLFOLLQNKHCPOGNSAPAGWRPMSPPSPFKI-QPSMRGRD--PTH 241

RESULT 6
US-10-116-051-10
Sequence 10, Application US/10116051
Patent No. US20020146791A1
GENERAL INFORMATION:
APPLICANT: Olsen et al.
TITLE OF INVENTION: CORPUSCLES OF STANNIUS PROTEIN, STANNIOCALCIN
FILE REFERENCE: PFI08P1C1
CURRENT APPLICATION NUMBER: US/10/116,051
CURRENT FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: 09/312,610
PRIOR FILING DATE: 1999-05-17
PRIOR APPLICATION NUMBER: 08/431,117
PRIOR FILING DATE: 1995-04-28
PRIOR APPLICATION NUMBER: 08/208,005
PRIOR FILING DATE: 1994-03-08
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn version 3.1
SEQ ID NO 10
LENGTH: 204
TYPE: PRT
ORGANISM: Oncorhynchus kisutch
US-10-116-051-10

Query Match 52.1%; Score 660.5; DB 12; Length 204;
Best Local Similarity 60.8%; Pred. No. 1.2e-58;
Matches 118; Conservative 38; Mismatches 37; Indels 1; Gaps 1;

QY 11 LVISASATHEAEQNDVSPKRSRVAQAQNSAEVVRCLNSALQVCGGAFACLNSTCDTGM 70
DB LVISATATFTDPEEA-SPRRARFSSNSPSDVARCLNGALAVCGGTFACLNSTCDTGM 70

QY 71 YDICKSFLYSAAKFTQKAFVKESLKCIAANGVTSKVFLAIRRCSTFORMIAEVOEECY 130
DB HDICQLFPHTAATNTQKTFVKESLRCIAANGVTSKVFTIRRCGVFQRMISEVOEECY 130

QY 131 KLVNCSIAKRNPETAEVVLQPNHFSNRYNRLVRSLLCEDEDTVSTIRDSLMEXIGPNM 190
DB 131 RLDICGVARSNPEAIGEVVQVPAHFPPNRYSTLLQSLACDEETVAVVRAGLVARLGPDM 190

QY 191 ASLPHILOTDHCAQ 204
DB 191 ETLFOLLQNKHCPO 204

RESULT 7
US-09-361-736-9
Sequence 9, Application US/09361736
Patent No. US20020102634A1
GENERAL INFORMATION:
APPLICANT: OLSEN, ET AL.
TITLE OF INVENTION: Human Stanniocalcin-alpha
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/361,736
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/460,529

```

; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-334 (PF143)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 170 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
US-09-361-736-9

Query Match 49.5%; Score 628; DB 10; Length 170;
Best Local Similarity 66.5%; Pred. No. 1.8e-55;
Matches 113; Conservative 30; Mismatches 27; Indels 0; Gaps 0;

QY 28 SPRKSRVAQNAEVRCLNSALQVCGGAFACLENSTCDTDCMYDICKSFLYSAAKFDQTQ 87
Db 1 SPRTARFSSPSDVARCLNGALQVCGSFAFLDNTCTDGMHICRSFLHGAAKFDQTQ 60

QY 88 GKAFVKESLKIANGVTSKVFLAIRRCSTFFORMIAEVOECYSKLVNCSIAKRNPEAITE 147
Db 61 GKTFFVKESLKIANGVTSKVFLAIRRCSTFFORMIAEVOECYSKLVNCSIAKRNPEAITE 120

QY 148 VVQLPNHFNRYNRLVRSLLCEDETVSTIRDSLMKTIKGNMAGLFIHL 197
Db 121 VAQVPSQFPNRYSTLLQSLTCDDETVEQVRAGLVRLPEPMGVLFQLL 170

RESULT 8
US-09-864-761-37770
; Sequence 37770, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aecmics-X-1
; CURRENT APPLICATION NUMBER: US/09/864, 761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662

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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 37770
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC012119.1
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN HEL100, SIGNAL = 2.4
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.8
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.8
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.4
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.1
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.8
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.2
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.7
; OTHER INFORMATION: SWISSPROT HIT: P52823, EVALUE 3.00e-35
; OTHER INFORMATION: EST_HUMAN HIT: AW954342.1, EVALUE 3.00e-34
US-09-864-761-37770

Query Match 28.2%; Score 358; DB 10; Length 70;
Best Local Similarity 100.0%; Pred. No. 7.8e-29;
Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 88 GKAFVKESLKIANGVTSKVFLAIRRCSTFFORMIAEVOECYSKLVNCSIAKRNPEAITE 147
Db 1 GKAFVKESLKIANGVTSKVFLAIRRCSTFFORMIAEVOECYSKLVNCSIAKRNPEAITE 60

QY 148 VVQLPNHFSN 157
Db 61 VVQLPNHFSN 70

RESULT 9
US-09-361-736-2
; Sequence 2, Application US/09361736
; Patent No. US20020102634A1
; GENERAL INFORMATION:
; APPLICANT: OLSEN, ET AL.
; NUMBER OF INVENTION: Human Stanniocalcin-alpha
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/361,736
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: 08/460,529

```

```

; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-334 (PF143)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
; US-09-361-736-2

Query Match 26.3%; Score 333.5; DB 10; Length 251;
Best Local Similarity 32.6%; Pred. No. 1.3e-25;
Matches 78; Conservative 43; Mismatches 89; Indels 29; Gaps 5;

QY 9 LVLVIS-----ASATHEAE-QNDSVSPKSRVAAQNSAEVVRCLNSALQVCGAFACL 60
DB 12 LALVLATPPARGTDATNPPEGPQDRESSQOKGRLSLQNTAEIQHCLVNAAGDVGCGVECF 71
QY 61 ENSTCDTDMYDICKSFLYSAAKFTDQKAFVKESLKCITANGVTSKVFLAIRRCSTFORM 120
DB 72 ENNSCEIRGLHGICMTFLHAGKFDQAGKSFIDKALKCAHALRHRFGCISRKCPAIREM 131
QY 121 IAEVQEECYKLVNCSIAKNPEATEVQVLPNPHSNRYNRLVRSLLCEDEDTVTIRD 180
DB 132 VSQLRGCTLKHDLCAAGENTRVIVEMTHFDLLHGPYDVLNLLTCGEEVKEAITH 191
QY 181 SLMEKIGPNMASLFILOTDHCAQ-----THP-----RADFNRRRTNEQP 220
DB 192 SVQVQCEQNWGSLCSIL--SFCTSDIQKPTAPPERPQVDRTKLSRAHHGGRTPSPR 248

RESULT 10
US-10-116-051-9
; Sequence 9, Application US/10116051
; Patent No. US20020146791A1
; GENERAL INFORMATION:
; APPLICANT: Olsen et al.
; TITLE OF INVENTION: CORPUSCLES OF STANNIUS PROTEIN, STANNIOCALCIN
; FILE REFERENCE: PF108PD1C1
; CURRENT APPLICATION NUMBER: US/10/116,051
; PRIOR FILING DATE: 2002-04-05
; PRIOR FILING DATE: 1999-05-17
; PRIOR FILING DATE: 08/431,117
; PRIOR FILING DATE: 1995-04-28
; PRIOR FILING DATE: 08/208,005
; PRIOR FILING DATE: 1994-03-08
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 9
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Oncomorhynchus kisutch
; US-10-116-051-9

Query Match 23.9%; Score 303; DB 12; Length 118;
Best Local Similarity 54.9%; Pred. No. 5.5e-23;
Matches 96; Conservative 8; Mismatches 9; Indels 62; Gaps 20;

QY 28 SPKSRVAAQNSAEVVRCLNSALQVCGAFACLENSTCDTDMYDICKSFLYSAAKFTQ 87
DB 5 SPRR-----VRCLNAL--VCGG-FACLENSTCDTDMYDICKSFLYSAAKFTQ 42
QY 88 GKAFVKESLKIANGVTSKVFLAIRRCSTFORMIAEVEQECYKLVNCSIAKNPEATE 147
DB 43 GK-FVKESL-CIANGVTSKVF--IRRC--FORMI-EVQEECYKLVNCSIAKNPEATE 87

; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-334 (PF143)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
; US-09-361-736-2

Query Match 26.3%; Score 333.5; DB 10; Length 251;
Best Local Similarity 32.6%; Pred. No. 1.3e-25;
Matches 78; Conservative 43; Mismatches 89; Indels 29; Gaps 5;

QY 9 LVLVIS-----ASATHEAE-QNDSVSPKSRVAAQNSAEVVRCLNSALQVCGAFACL 60
DB 12 LALVLATPPARGTDATNPPEGPQDRESSQOKGRLSLQNTAEIQHCLVNAAGDVGCGVECF 71
QY 61 ENSTCDTDMYDICKSFLYSAAKFTDQKAFVKESLKCITANGVTSKVFLAIRRCSTFORM 120
DB 72 ENNSCEIRGLHGICMTFLHAGKFDQAGKSFIDKALKCAHALRHRFGCISRKCPAIREM 131
QY 121 IAEVQEECYKLVNCSIAKNPEATEVQVLPNPHSNRYNRLVRSLLCEDEDTVTIRD 180
DB 132 VSQLRGCTLKHDLCAAGENTRVIVEMTHFDLLHGPYDVLNLLTCGEEVKEAITH 191
QY 181 SLMEKIGPNMASLFILOTDHCAQ-----THP-----RADFNRRRTNEQP 220
DB 192 SVQVQCEQNWGSLCSIL--SFCTSDIQKPTAPPERPQVDRTKLSRAHHGGRTPSPR 248

RESULT 11
US-09-828-062-8
; Sequence 8, Application US/09828062
; Publication No. US20030097675A1
; GENERAL INFORMATION:
; APPLICANT: COSTA E SILVA, OSWALDO DA
; APPLICANT: BOHNET, HANS J.
; APPLICANT: VAN THIELEN, NOCHA
; APPLICANT: CHEN, ROUYING
; APPLICANT: SARRIA-MILLAN, RODRIGO
; TITLE OF INVENTION: CELL CYCLE STRESS-RELATED PROTEINS AND METHODS OF USE
; TITLE OF INVENTION: IN PLANTS
; FILE REFERENCE: 16313-0031
; CURRENT APPLICATION NUMBER: US/09/828,062
; PRIOR FILING DATE: 2001-08-20
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 8
; LENGTH: 901
; TYPE: PRT
; ORGANISM: Physcomitrella patens
; US-09-828-062-8

Query Match 7.2%; Score 91; DB 9; Length 901;
Best Local Similarity 20.2%; Pred. No. 1.9;
Matches 47; Conservative 40; Mismatches 98; Indels 48; Gaps 7;

QY 16 SATHEAEONDSVSPKSRVAAQNSAEVVRCLNSALQVCGAFACLENSTCDTDMYDICK 75
DB 282 ASVHMRELNPSSDIDKLVSVKGM-----VIRCSIIPEIKGAFKCL-----VCG 325
QY 76 SFLYSAARFDTQKAFVKESLKCITANGVTSKVFLAI--RRGSTFORMIAEVEQECYKLVN 133
DB 326 ----HSPPLVTIVKGRVEEPTRCPECAARNAMSLIHNRCITFANKQIVRLQE----- 374
QY 134 VCSIAKNPEATEVQVLPNPHSNRYNRLVRSLLCEDEDTVTSTIRDSLMEKIGPNMASL 193
DB 375 -----TPDAIPE-GETPHTVSMCLYNTMDAVKPGDRIEVTGVFKAMAVRVGNQRTL 426
QY 194 PHILOTDHCAQTHPRADFNRRRTNEPQKLVLLNRLRGEEDSPSHIKRTSHES 246
DB 427 RALYKTYIDCVHVKKSDRGRLQTEPDM-----EMDKENDMYAGYHES 468

RESULT 12
US-09-419-305-1
; Sequence 1, Application US/09419305
; Patent No. US20020102696A1
; GENERAL INFORMATION:
; APPLICANT: MARUTA, Kazuhiko
; APPLICANT: KUBOTA, Michio
; APPLICANT: SUGIMOTO, Toshiyuki
; TITLE OF INVENTION: RECOMBINANT THERMOSTABLE ENZYME WHICH
; TITLE OF INVENTION: FORMS NON-REDUCING SACCHARIDE FROM REDUCING AMYLACEOUS
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street N.W. Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
```

COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/419,305
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/505,448
 FILING DATE: 21-JUL-1994
 APPLICATION NUMBER: JP 190183/1994
 FILING DATE: 21-JUL-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 189706/1995
 FILING DATE: 04-JUL-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Browdy, Roger L.
 REGISTRATION NUMBER: 25,618
 REFERENCE/DOCKET NUMBER: MARUTA-3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 628-5197
 TELEFAX: (202) 737-3528
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 720 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-419-305-1

Query Match 6.4%; Score 81; DB 10; Length 720;
 Best Local Similarity 24.2%; Pred. No. 14;
 Matches 38; Conservative 22; Mismatches 45; Indels 52; Gaps 9;
 QY 86 TQKAPVKESLKIANGVTSKVP-LAIR-----CSTFORMIA-EVQS 126
 Db 299 TAEKISISIKKIAQIIIDELFSYEVKSLASQLGISYIDRLDYLSCIDVYRTYANQIVK 358
 QY 127 ECYKSLNVCISAKRNPETATVVO-LPNHFSNRY-----YNRLVRSLECEDTSTVI 178
 Db 359 ECDKNEIEEATRNRPETATVVO-LPNHFSNRY-----YNRLVRSLECEDTSTVI 413
 QY 179 RDSLMEKIGPNMASLFIHQDHCATHPRADFNRRR 215
 Db 414 ---RYKISPDQ---FHV-----FNQKR 430

RESULT 13
 US-09-736-968A-110
 ; Sequence 110, Application US/09736968A
 ; Patent No. US20020169283A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lu, Peter
 ; APPLICANT: Garman, Jonathan David
 ; APPLICANT: Candia III, Albert Frederick
 ; APPLICANT: Arbor Vita Corporation
 ; TITLE OF INVENTION: CLASP-7 Transmembrane Protein
 ; FILE REFERENCE: 020054-000611US
 ; CURRENT APPLICATION NUMBER: US/09/736,968A
 ; CURRENT FILING DATE: 2000-12-13
 ; PRIOR APPLICATION NUMBER: US 60/160,860
 ; PRIOR FILING DATE: 1999-10-21
 ; PRIOR APPLICATION NUMBER: US 60/162,498
 ; PRIOR FILING DATE: 1999-10-29
 ; PRIOR APPLICATION NUMBER: US 60/170,453
 ; PRIOR FILING DATE: 1999-12-13
 ; PRIOR APPLICATION NUMBER: US 60/176,195
 ; PRIOR FILING DATE: 2000-01-14
 ; PRIOR APPLICATION NUMBER: US 60/182,296
 ; PRIOR FILING DATE: 2000-02-14
 ; PRIOR APPLICATION NUMBER: US 09/547,276
 ; PRIOR FILING DATE: 2000-04-11
 ; PRIOR APPLICATION NUMBER: US 60/196,267

; PRIOR FILING DATE: 2000-04-11
 ; PRIOR APPLICATION NUMBER: US 60/196,460
 ; PRIOR FILING DATE: 2000-04-11
 ; PRIOR APPLICATION NUMBER: US 60/196,527
 ; PRIOR FILING DATE: 2000-04-11
 ; PRIOR APPLICATION NUMBER: US 60/196,528
 ; PRIOR FILING DATE: 2000-04-11
 ; PRIOR APPLICATION NUMBER: US 09/687,837
 ; PRIOR FILING DATE: 2000-10-13
 ; PRIOR APPLICATION NUMBER: US 60/240,503
 ; PRIOR FILING DATE: 2000-10-13
 ; PRIOR APPLICATION NUMBER: US 60/240,508
 ; PRIOR FILING DATE: 2000-10-13
 ; PRIOR APPLICATION NUMBER: US 60/240,539
 ; PRIOR FILING DATE: 2000-10-13
 ; PRIOR APPLICATION NUMBER: US 60/240,543
 ; PRIOR FILING DATE: 2000-10-13
 ; NUMBER OF SEQ ID NOS: 115
 ; SOFTWARE: Patent In Ver. 2.1
 ; SEQ ID NO 110
 ; LENGTH: 2180
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: human CLASP-1
 US-09-736-968A-110
 Query Match 6.3%; Score 80; DB 9; Length 2180;
 Best Local Similarity 21.7%; Pred. No. 84;
 Matches 40; Conservative 30; Mismatches 76; Indels 38; Gaps 6;
 QY 68 DGMVDICKSFLYSAAKFTDQ---KAFVKESLKIANGVTSKVPFLAIRRCSTFORMIAEV 124
 Db 831 DGGKPLFKVTFVSTVNTQDPHVNAFQECQK-----REKMSQSPTSNF 876
 QY 125 QEECYKSLNVCISAKRNPETATVVO-LPNHFSNRY-----YNRLVRSLECEDTSTVIRDSLME 184
 Db 877 IRSCKNLLNV-----EKIHAIMSFILNQLFKVLVQNEDEIT---TVT 920
 QY 185 KIGPNMASLFIHQDHCATHPRADFNRRRNEPQKLVKLLRNLRG---EEDSPS--HI 239
 Db 921 RVLDPDIVAKCHEEQLDHSVQSIKVFVKTRACKERPVEDLAKNVTGLLKNDSPTVKHV 980
 QY 240 KRTS 243
 Db 981 LKHS 984
 RESULT 14
 US-09-736-969A-96
 ; Sequence 96, Application US/09736969A
 ; Patent No. US20020068302A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lu, Peter
 ; APPLICANT: Garman, Jonathan David
 ; APPLICANT: Candia III, Albert Frederick
 ; APPLICANT: Arbor Vita Corporation
 ; TITLE OF INVENTION: CLASP-4 Transmembrane Protein
 ; FILE REFERENCE: 020054-000411US
 ; CURRENT APPLICATION NUMBER: US/09/736,969A
 ; CURRENT FILING DATE: 2000-12-13
 ; PRIOR APPLICATION NUMBER: US 60/160,860
 ; PRIOR FILING DATE: 1999-10-21
 ; PRIOR APPLICATION NUMBER: US 60/162,498
 ; PRIOR FILING DATE: 1999-10-29
 ; PRIOR APPLICATION NUMBER: US 60/170,453
 ; PRIOR FILING DATE: 1999-12-13
 ; PRIOR APPLICATION NUMBER: US 60/176,195
 ; PRIOR FILING DATE: 2000-01-14
 ; PRIOR APPLICATION NUMBER: US 60/182,296
 ; PRIOR FILING DATE: 2000-02-14
 ; PRIOR APPLICATION NUMBER: US 09/547,276
 ; PRIOR FILING DATE: 2000-04-11

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OM protein - protein search, using sw model

Run on: June 12, 2003, 19:48:33 ; Search time 44 Seconds
(without alignments)
539.664 Million cell updates/sec

Title: US-09-705-500A-3

Perfect score: 1268
Sequence: 1 MLQNSAVLLVLVISASATHE.....NLRGEDSPSHKRTSHESA 247

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 73.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	680.5	53.7	263	2 A54648	stanniocalcin prec
2	662.5	52.2	256	2 I51197	stanniocalcin - co
3	354	27.9	302	2 J20357	stanniocalcin homo
4	150	11.8	40	2 B60841	teleocalcin - coho
5	149	11.8	40	2 A60841	teleocalcin - sock
6	123	9.7	33	2 S06337	teleocalcin - rain
7	102	8.0	473	2 T04799	hypothetical prote
8	94	7.4	1105	2 T18295	Ap-3 adaptor compl
9	90.5	7.1	289	2 T50776	hypothetical prote
10	90.5	7.1	783	2 T38690	probable regulator
11	89.5	7.1	1126	2 T01491	ubiquitin-protein
12	89	7.0	305	2 T08121	peroxidase (EC 1.1
13	88	6.9	473	2 T45954	hypothetical prote
14	87.5	6.9	1465	2 S45628	DNA-directed DNA p
15	86	6.8	470	2 H72097	mg++ transporter (
16	86	6.8	470	2 F85526	Mg++ transporter (
17	86	6.8	510	2 T45952	hypothetical prote
18	86	6.8	556	2 S51858	probable membrane
19	86	6.8	581	2 S58201	hypothetical prote
20	83	6.5	250	2 S30584	hypothetical prote
21	83	6.5	250	2 D62115	conserved hypothet
22	83	6.5	365	2 T06693	hypothetical prote
23	83	6.5	1093	2 T50652	AP-3 complex beta3
24	83	6.5	1094	2 T50651	AP-3 complex beta3
25	82.5	6.5	869	2 A88710	protein C43G2.2 (i
26	82.5	6.5	1483	2 S30015	hypothetical prote
27	82.5	6.5	1757	2 T05204	hypothetical prote
28	82.5	6.5	2335	2 T40186	probable phosphati
29	82.5	6.5	2535	2 T04824	hypothetical prote

conserved hypothet
hypothetical prote
hypothetical prote
conserved hypothet
lactotransferin p
hypothetical prote
glycosyltransferas
FAB1 protein homol
ankyrin 3, long sp
probable endonucle
major envelope gly
protein gp64 - Org
Ca2+-transporting
Ca2+-transporting
probable membrane
zinc finger protei

ALIGNMENTS

RESULT 1

A54648

stanniocalcin precursor - Australian eel

N/Alternate names: Stannius corpuscle secretory protein

C/Species: Anguilla australis (Australian eel)

C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 07-May-1999

C/Accession: A54648

R/Butkus, A.; Roche, P.J.; Fernley, R.T.; Haralambidis, J.; Penschow, J.D.; Ryan, G.B.;

Mol. Cell. Endocrinol. 54, 123-133, 1987

A/Title: Purification and cloning of a corpuscles of Stannius protein from Anguilla austri

A/Reference number: A54648; MUID:88083961; PMID:3319739

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-263 <BUT>

F/1-17/Domain: signal sequence #status predicted <SIG>

F/18-263/Product: stanniocalcin #status predicted <MAT>

Query Match 53.7%; Score 680.5; DB 2; Length 263;

Best Local Similarity 61.4%; Pred. No. 2.4e-51;

Matches 124; Conservative 41; Mismatches 36; Indels 1; Gaps 1;

Qy 1 MLQNSAVLLVLVISASATHEAQNDVSVPKRSVAQAQNSALQVCGGAFACL 60
Db 1 MLRNSGLILTLVL-VTAAVEQDESEPLSPRTARFSASSPSDVARCLNGALQVCGSFAACL 59
Qy 61 ENSTCDTDGMYDICKSFYLSAAKFTDQKAFVKESLKCIAANGVTSKVFLAIRCSTFORM 120
Db 60 DNSTCNTDGMHEICRSEFLHGAAKFTDQKTFVKESLKCIAANGITSKVFLTIRCCSFQKM 119
Qy 121 IAEVQECYKLVNCSIAKRNPEAITVEVQLPNHFSNRYNRLVRSLLCEDEDTVTSTIRD 180
Db 120 ISEVQECYKLVNCSIAKRNPEAITVEVQLPNHFSNRYNRLVRSLLCEDEDTVTSTIRD 179
Qy 181 SLMEKIGPNMASLFIHLQTDHC 202
Db 180 GLVSRLEPEMGVLFQLLQTRAC 201

RESULT 2

I51197

stanniocalcin - coho salmon

C/Species: Oncorhynchus kisutch (coho salmon)

C/Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000

C/Accession: I51197

R/Wagner, G.F.; Dimattia, G.E.; Davie, J.R.; Copp, D.H.; Friesen, H.G.

Mol. Cell. Endocrinol. 90, 7-15, 1992

A/Title: Molecular cloning and cDNA sequence analysis of coho salmon stanniocalcin.

A/Reference number: I51197; MUID:93246046; PMID:1363790

A/Accession: I51197

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A;Residues: 1-256 <WAG>
A;Cross-references: GB:S59519; NID:G299926; PIDN:AAB26419.1; PID:G299927

Query Match 52.2%; Score 662.5; DB 2; Length 256;
Best Local Similarity 53.4%; Pred. No. 8.3e-50;
Matches 125; Conservative 46; Mismatches 54; Indels 9; Gaps 4;

QY 11 LVISATHEAEQNDVSVPKSRVAQNSAEVVRCLNSALQVCGGAFACLENSTCDTDGM 70
DB 12 LVLGTAFTDTPAEA-SPPRARFSSNSPSDVARCLNGALAVCGGTFFACLENSTCDTDGM 70

QY 71 YDICKSFLYSAAKFTQGAFAFKESLKIANGVTSKVFLAIRRCSTFTORMIAEVEQECYS 130
DB 71 HDICQLFFHTAATFTQGTTFVKESLRLCIANGVTSKVFTIRRCGVQFMISEVQECYS 130

QY 131 KLVNCSIAKENPEATEVVLNPHFSNRYNRLVSLLECDSDTSTIRDSLMEKIGPNM 190
DB 131 RLDDICGVARSNPEAIGEVVQVFAHPNRYYSLLQSLACDETVAVVRAGLVARLGPDM 190

QY 191 ASLFILQTDHCAQTHPRADFN-----RRRTNEPQKLKVLNRLNRGEEDSPSHI 239
DB 191 ETLFQLLQNKHCPCQSNQCPNSAPAGWRWPMGSPSPFKI-QPSMRGRD--PTRL 241

RESULT 3
JE0357
stanniocalcin homolog - human
N;Alternate names: STC2
C;Species: Homo sapiens (man)
C;Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 21-Jul-2000
A;Title: Molecular cloning of a second human stanniocalcin homologue (STC2).
A;Reference number: JE0357; MUID:98440784; PMID:9753616
R;Ishibashi, K.; Miyamoto, K.; Takekani, Y.; Morita, K.; Takeda, E.; Sasaki, S.; Imai, M.
Biochem. Biophys. Res. Commun. 250, 252-258, 1998
A;Comment: This protein suppressed expression of renal sodium/phosphate cotransporter.
C;Genetics: JE0357
A;Molecule type: mRNA
A;Residues: 1-302 <ISH>
A;Cross-references: DDBJ:AB012664; NID:G3702223; PIDN:BAA33489.1; PID:G3702224
C;Comment: This protein suppressed expression of renal sodium/phosphate cotransporter.
A;Introns: 51/1 98/3 169/2

Query Match 27.9%; Score 354; DB 2; Length 302;
Best Local Similarity 32.4%; Pred. No. 4.7e-23;
Matches 83; Conservative 45; Mismatches 102; Indels 26; Gaps 4;

QY 9 LVLVTS-----ASATHEAE-QNDVSVPKSRVAQNSAEVVRCLNSALQVCGGAFACL 60
DB 12 LALVLATFDPARGTDATNPPEGPDQRSSQKGRSLQNTAEIQHCLVNAVGVCGVPECF 71

QY 61 ENSTCDTDGMVDICKSFLYSAAKFTQGAFAFKESLKIANGVTSKVFLAIRRCSTFORM 120
DB 72 ENNSCEIRGLHGICMTFLHNAGKFAQGGKSFIDKALKCKAHARHRCGICSRKCPAIREM 131

QY 121 IAEVEBECYSKLVNCSIAKENPEATEVVLNPHFSNRYNRLVSLLECDSDTSTIRSD 180
DB 132 VSQLORECYLKHDLCAQAQENTRVIVEMHFKDILLHPYVDLVNLLTTCGEVKEATH 191

QY 181 SLMEKIGPNMASLFILQ-TDCAQTHPRADFNRRRTNEPQKL----- 222
DB 192 SVQVQCEQNWGSLCSILSPTSIAIQKPTTAPPERQVDRTKLSRAHGEAGHLPPEPS 251

QY 223 KVLNRLNRGEEDSPSH 238
DB 252 RETGRGAKGERGSKSH 267

RESULT 4
B60841
teleocalcin - coho salmon (fragment)
C;Species: Oncorhynchus kisutch (coho salmon)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 30-Sep-1993

C;Accession: B60841
R;Wagner, G.F.; Fenwick, J.C.; Park, C.M.; Milliken, C.; Copp, D.H.; Friesen, H.G.
Gen. Comp. Endocrinol. 72, 237-246, 1988
A;Title: Comparative biochemistry and physiology of teleocalcin from sockeye and coho sal
A;Reference number: A60841; MUID:89065334; PMID:3197944
A;Accession: B60841
A;Molecule type: protein
A;Residues: 1-40 <WAG>
C;Comment: This glycoprotein hormone from the corpuscles of Stannius regulates calcium ut
C;Keywords: disulfide bond; glycoprotein; hormone

Query Match 11.8%; Score 150; DB 2; Length 40;
Best Local Similarity 66.7%; Pred. No. 1.9e-06;
Matches 26; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 35 AAQNSAEVVRCLNSALQVCGGAFACLENSTCDTDGMVDI 73
DB 2 SSNSPSDVARCLNGALAVCGGTFFACLEXSTCDTDGMHDI 40

RESULT 5
A60841
teleocalcin - sockeye salmon (fragment)
C;Species: Oncorhynchus nerka (sockeye salmon)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 30-Sep-1993
C;Accession: A60841
R;Wagner, G.F.; Fenwick, J.C.; Park, C.M.; Milliken, C.; Copp, D.H.; Friesen, H.G.
Gen. Comp. Endocrinol. 72, 237-246, 1988
A;Title: Comparative biochemistry and physiology of teleocalcin from sockeye and coho sal
A;Reference number: A60841; MUID:89065334; PMID:3197944
A;Accession: A60841
A;Molecule type: protein
A;Residues: 1-40 <WAG>
C;Comment: This glycoprotein hormone from the corpuscles of Stannius regulates calcium ut
C;Keywords: disulfide bond; glycoprotein; hormone

Query Match 11.8%; Score 149; DB 2; Length 40;
Best Local Similarity 76.5%; Pred. No. 2.3e-06;
Matches 26; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 40 AEVVRCLNSALQVCGGAFACLENSTCDTDGMVDI 73
DB 7 SDVARCLNGALDVCGGTFFACLEXSTCDTDGMHDI 40

RESULT 6
S06337
teleocalcin - rainbow trout (fragment)
N;Alternate names: hypocalcin
C;Species: Oncorhynchus mykiss (rainbow trout)
C;Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 18-Jun-1993
C;Accession: S06337
R;Lafaber, F.P.J.G.; Hanssen, R.G.J.M.; Choy, Y.M.; Flik, G.; Hermann-Erlee, M.P.M.; Par
Gen. Comp. Endocrinol. 69, 19-30, 1988
A;Title: Identification of hypocalcin (teleocalcin) isolated from trout stannius corpuscul
A;Reference number: S06337; MUID:88196801; PMID:3360288
A;Accession: S06337
A;Molecule type: protein
A;Residues: 1-33 <LAF>
A;Note: 7-Glu was also found
C;Keywords: dimer; glycoprotein; hormone
F;29/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 9.7%; Score 123; DB 2; Length 33;
Best Local Similarity 65.6%; Pred. No. 0.00032;
Matches 21; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 35 AAQNSAEVVRCLNSALQVCGGAFACLENSTCD 66
DB 2 SSNSPSDVARCLNGALAVCGGTFFACLENSTCD 33

RESULT 7

T04799
Hypothetical protein F10M23.100 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-Jun-1999
C:Accession: T04799
R:Bevan, M.; Lecharny, A.; Chedfor, F.; Krivitzky, M.; Kreis, M.; Hoheisel, J.; Mewes, H.
submitted to the Protein Sequence Database, February 1999
A:Reference number: Z15385
A:Accession: T04799
A:Molecule type: DNA
A:Cross-references: EMBL:AL035440
A:Experimental source: cultivar Columbia; BAC clone F10M23
C:Genetics:
A:Map position: 4
A:Introns: 24/3; 92/3; 184/3; 256/3; 308/3; 412/3
A:Note: F10M23.100

Query Match 8.0%; Score 102; DB 2; Length 473;
Best Local Similarity 21.0%; Pred. No. 0.49;
Matches 50; Conservative 43; Mismatches 67; Indels 78; Gaps 11;

QY 26 SVSPKRSVAQAQSAEVVRCVCLNSALQVCGGAPACLENSTCDT----DGMVDICKSF-LYS 80
DB 50 NYKKKVELAAKSRALQTLSD-----ATVELNLITLALGEKSYIDICDSMLFP 100
QY 81 AAKFTDQKAFVKESLKCIA-----ATVELNLITLALGEKSYIDICDSMLFP 102
DB 101 LQPDKTSGT--IKEQLSALAPALEQLWQKEERAFSDVQSQIQICEETAGLNGPH 158
QY 103 VTSKVFPLAIRCSTFORMIAEVQECYSKLV-----NVCSIAKRN-PEAITEV-- 148
DB 159 VVDETDLKRLDDPQRLQELQKESDRLOKVLFEVSTVHDLCAVRLDFLSTVTEVHP 218
QY 149 -----VQLPHFNGRYNRYNRLVRSLLCEDEDTVSTIRDSLMKIGPNWASIFHLQ 199
DB 219 SLDEANGVQTKS--ISNETLRLAKTLVTLKEDQMORLKK--LQELATQTLDLNLM 273

RESULT 8
T18295
Ap-3 adaptor complex beta3A chain - mouse
C:Species: Mus musculus (house mouse)
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T18295
R:Feng, L.; Seymour, A.B.; Jiang, S.Y.; To, A.; Peden, A.A.; Novak, E.K.; Zhen, L.; Rusi
Hum. Mol. Genet. 8, 323-330, 1999
A:Title: The beta3A subunit gene (Ap3b1) of the AP-3 adaptor complex is altered in the m
A:Reference number: Z18864; PMID:99135912; PMID:9931340
A:Accession: T18295
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1105 <PEP>
A:Cross-references: EMBL:AF103809; NID:G3885987; PID:G3885988; PIDN:AAC783338.1
A:Experimental source: strain C3H/HeJ
C:Genetics:
A:Gene: Ap3b1
A:Map position: 13

Query Match 7.4%; Score 94; DB 2; Length 1105;
Best Local Similarity 21.2%; Pred. No. 6.5;
Matches 55; Conservative 40; Mismatches 104; Indels 60; Gaps 11;

QY 1 MLQNSAVLLLVISASATHEAQNDVSVPKRSRVAQAQSAEVVRCVCLNSALQVCGGAPAC 60
DB 308 LQNSAAVVAQVAYVH-----ISPKSE--AGVTSKSLVRLRSNRREVQIVLQNI 358
QY 61 ENSTCDTDMVD-ICKSFYSAAKFDTQKAFVKESLKCIANGVTSKVFL----- 109
DB 359 ATMSIERKGMPEPYLKSF-YVRSSTPTMTKTLKLEILNLANEANISTLLREFQTVRSQ 417
QY 110 -----AIRRSTQRMIAEVQECYSKLVNVCSTAKNPEAITE---VVLQPNHFS 156

DB 418 DKQFAAATQITIGRCAT---SISEFTETCFNGL-VCLLSNRDEIVVAESVVVVIKKLQMQ 473
QY 157 NRYNRLVRSLE-CDEDTVSTIRDSLMKIGPNWASIFHLQTDHCAQTHPRADFNRR 215
DB 474 PAQHGEEIRHMAKFLDSITVPVARASILWLIGEN-----CERVPKIA----- 515
QY 216 TNEPQKLVLLRNURGED 234
DB 516 ---PDVLRKMAKSTSEDD 531

RESULT 9
T50776
Hypothetical protein [imported] - Vitis vinifera
C:Species: Vitis vinifera
C>Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 21-Jul-2000
C:Accession: T50776
R:Matsumoto, S.; Dry, I.B.; Thomas, M.
DNA Seq. 8, 109-112, 1997
A:Title: Nucleotide sequence of grapevine (Vitis vinifera) cDNA similar to SNAP proteins.
A:Reference number: Z25233
A:Accession: T50776
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-289 <MAT>
A:Cross-references: EMBL:AB001375; PIDN:BAAL19246.1
A:Experimental source: strain Shiraz

Query Match 7.1%; Score 90.5; DB 2; Length 289;
Best Local Similarity 19.9%; Pred. No. 2.7;
Matches 41; Conservative 33; Mismatches 95; Indels 37; Gaps 5;

QY 8 LLVLVIGASATHEAQNDVSVPKRSRVAQAQSAEVVRCVCLNSALQVCGGAPACLENSTCDT 67
DB 59 LSTVIQSSDSKHEAAQ--AYADAGHCYKTSKAKAISCLEQA-----AYLFLDNGRFNM 110
QY 68 DG-----MYDICKSFLYSAAKFDQKAFVKESLKCIANGVTSKVFLAIRCSTQ 119
DB 111 AGKYKETAELYLEQNFQEAIIYFEKAADIYQSEEAATTAANQCNKAKVAQFAAQLEQYQK 170
QY 120 MIAEVQECYSKLVNVCSTAKNPEAITEVVL-----VCSIAKRNPEAITEVVL-----PNHFSNR 158
DB 171 AIQYVEDIGRPSLNLLKYGKGLHLLNAGICQLCKGDVVVAITNALDRYQEMDPTFSGTR 230
QY 159 YNRLVRSLLCEDEDTVSTIRDSLMK 184
DB 231 EYLLVLDLAAVDEEDVVKFTDAVKE 256

RESULT 10
T38690
Probable regulatory protein - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jun-2000
C:Accession: T38690
R:Brown, D.; Churcher, C.M.; Wood, V.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, September 1997
A:Reference number: Z21805
A:Accession: T38690
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-783 <BRQ>
A:Cross-references: EMBL:Z99568; PIDN:CAB16735.1; GSPDB:GN00066; SPDB:SPAC3C7.04
A:Experimental source: strain 972h-; cosmid C3C7
C:Genetics:
A:Map position: 1
A:Superfamily: unassigned GAL4-type zinc cluster proteins; GAL4 zinc binuclear cluster hc
F:35-71/Domain: GAL4 zinc binuclear cluster homology <GL4>

Query Match 7.1%; Score 90.5; DB 2; Length 783;
Best Local Similarity 23.3%; Pred. No. 8.7;
Matches 56; Conservative 34; Mismatches 87; Indels 63; Gaps 12;

[illegible]

RESULT 11

T01491

ubiquitin-protein ligase homology F1707.15 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 12-Feb-1999 #sequence [revision 12-Feb-1999 #text_change 04-Mar-2000

C:Accession: T01491

R:Vysotskaia, V.S.; Schwartz, J.R.; Toriumi, M.; Yu, G.; Kwan, A.; Oji, O.; Liu, S.; Li, rtz, D.; Li, Y.; Palm, C.J.; Shinn, P.; Sun, H.; Davis, R.W.; Ecker, J.R.; Federspiel, N

A:Reference number: Z14334

A:Description: Arabidopsis thaliana chromosome 1 BAC F1707 sequence.

A:Reference number: Z14334

A:Accession: T01491

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1126 <VYS>

A:Cross-references: EMBL:AC003671; NID:Q2833627; PID:g3176690; GSPDB:GN00059; ATSP:F1707

A:Experimental source: cultivar Columbia

C:Genetics:

A:Gene: ATSP:F1707.15

A:Map position: 1

A:Introns: 118/3; 224/3; 292/1; 373/3; 457/2; 826/3; 875/3; 902/3; 1057/3; 1093/2

C:Superfamily: ubiquitin-protein ligase homology

F:756-1120/Domain: ubiquitin-protein ligase homology <UBI>

Query Match	7.1%;	Score 89.5;	DB 2;	Length 1126;
Best-Local Similarity	22.1%;	Pred. No. 16;		
Matches	46;	Conservative 39;	Mismatches 76;	Indels 47; Gaps 8
QY	14	SASATHEAENDSVSPKSRVAAQNSAEVVRCLNSALQVCGAFACLENSTCD-	-----	66
DB	412	SSETQDAESELVARRK-----NCAEL---YNI FLQLP-----QSDLCNLCMLGY	455	
QY	67	----TGMYDICKFYLYSAAKFTDQGA FVKESLKC IANGVTSKVFIAIRRCSTFORMIAE	123	
DB	456	EGLSDKIYSLAGEVLKLAADVTHRKFTFKELSELASGLSSSTVRVLA TSLSTTKQV---	512	
QY	124	VQEECVSKLVNCSIAKRNP EATEVVLQPNHFSNRYNRLVRSILCEDDTVSTIR---	179	
DB	513	-----SQNTCSMA---GASILRVQLVLSLSTTIDDSNVGTDKETDQEQNIMGLGV	562	
QY	180	--DSLMEKIGPNMASLPHILOTDHCAQT	205	
DB	563	ALEPLWQELGOCIS--MTELOLDHTAAT	588	

RESULT 12
T08121
peroxidase (EC 1.11.1.7) - flax (fragment)
C:Species: Linum usitatissimum (flax)
C:Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 04-Mar-2000
C:Accession: T08121
R:Omann, F.; Tyson, H.
submitted to the EMBL Data Library, February 1998
A:Description: cDNA sequence of a basic peroxidase (FLXPER4) in flax.
A:Reference number: Z16366

A:Accession: T08121
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-305 <OMA>
A:Cross-references: EMBL:AF049881; NID:G2944416; PIDN:AA05277.1; PID:G2944417
A:Experimental source: cv. Stormont Cirrus
C:Genetics:
A:Gene: PER4
C:Superfamily: peroxidase
C:Keywords: chromoprotein; heme; iron; metalloprotein; oxidoreductase
F:21-103/Disulfide bonds: #status predicted
F:50/Active site: Arg #status predicted
F:54,151/Binding site: heme iron (His) (axial ligands) #status predicted
F:56-61/Disulfide bonds: #status predicted
F:109-301/Disulfide bonds: #status predicted
F:188-213/Disulfide bonds: #status predicted

Query Match 7.0% Score 89; DB 2; Length 305;
Best Local Similarity 21.9%; Pred. No. 3.8;
Matches 57; Conservative
Indels 72; Gaps 15

[illegible]

RESULT 13
T45954
hypothetical protein F7J8.120 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 20-Jun-2000
C;Accession: T45954
R;Bevan, M.; Zimmermann, W.; Gruenewald, A.; Wambutt, R.; Bancroft, I.; Mewes,
submitted to the Protein Sequence Database, January 2000
A;Reference number: Z23018
A;Accession: T45954
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-473 <BEV>
A;Cross-references: EMBL:AL137189
A;Experimental source: cultivar Columbia; BAC clone F7J8
C;Genetics:
A;Map position: 5
A;Introns: 29/1; 428/3
A;Note: F7J8.120
C;Superfamily: Arabidopsis thaliana hypothetical protein F7J8.130

```

Query Match      6.9%; Score 88; DB 2; Length 473;
Best Local Similarity 22.6%; Pred. No. 7.9;
Matches 54; Conservative 42; Mismatches 103; Indels 40; Gaps 13

QY      27 VSPKRSVAAQNSAEVVRCLNSALQVCGGAFACLEN---STCD---TDGMVDICKS-FLY 79
      16 IDEKKNVLAEGACTIVRLIAKHKRSDPVITGCLRNLYTSVVDVLDLDFETACKQMLLY 75
QY      80 SAAKFDTQ GKAF-----VKSLKCIANGVTSKVFLAIRRCRCTFORMIAE---VOEEC-- 128

```


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OM protein - protein search, using sw model

Run on: June 12, 2003, 18:20:03 ; Search time 36 Seconds

(without alignments)
284.574 Million cell updates/sec

Title: US-09-705-500A-3

Perfect score: 1268

Sequence: 1 MLQNSAVLLVLVISASATHE.....NLRGEDSPSHIKTSHESA 247

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1268	100.0	247	1 STC1_HUMAN	P52823 homo sapien
2	1234	97.3	247	1 STC1_MOUSE	O55183 mus musculus
3	1231	97.1	247	1 STC1_RAT	P97574 rattus norv
4	682	53.8	250	1 STC_ANGAU	P18301 anguilla au
5	662.5	52.2	256	1 STC_ONCKI	Q08264 oncorhynch
6	662.5	52.2	256	1 STC_ONCMY	P43648 oncorhynch
7	617	48.7	179	1 STC_ONCKE	P43647 oncorhynch
8	354.5	28.0	296	1 STC2_MOUSE	O88452 mus musculus
9	354	27.9	302	1 STC2_HUMAN	O76061 homo sapien
10	352	27.8	302	1 STC2_MACNE	O97561 macaca neme
11	349	27.5	296	1 STC2_RAT	O970k8 rattus norv
12	181.5	14.3	197	1 STC2_CAVPO	P57675 cavia porce
13	156	12.3	40	1 STC2_ONCNE	P43649 oncorhynch
14	94	7.4	1105	1 A3B1_MOUSE	Q921t1 mus musculus
15	90.5	7.1	289	1 SNA4_VITVI	P33609 mus musculus
16	87.5	6.9	1465	1 DPOA_MOUSE	P33798 vitis vinif
17	86.5	6.8	509	1 VP67_NPVCF	P41717 choristoneu
18	86	6.8	581	1 YNM7_YEAST	O03124 saccharomyc
19	86	6.8	695	1 TRFL_HORSE	O77811 equus cabal
20	84.5	6.7	1451	1 DPOA_RAT	O89042 rattus norv
21	83	6.5	1094	1 A3B1_HUMAN	O00203 homo sapien
22	82.5	6.5	1483	1 UFDA_YEAST	P33202 saccharomyc
23	81.5	6.4	708	1 TRFL_BOVIN	P24627 bos taurus
24	81	6.4	4377	1 ANK3_HUMAN	Q12955 homo sapien
25	80	6.3	509	1 VP64_NPVOP	P13625 orgyia pseu
26	80	6.3	998	1 ECAR3_ARATH	Q8Y555 arabidopsis
27	79.5	6.3	708	1 TRFL_BUBBU	O77698 bubalus bub
28	79	6.2	440	1 V117_FOWPV	Q915a5 fallop vir
29	78.5	6.2	132	1 IL4_HORSE	P42202 equus cabal
30	78.5	6.2	708	1 TRFL_CAPHI	Q29477 capra hircu
31	78.5	6.2	1127	1 MDM1_YEAST	Q01846 saccharomyc
32	78	6.2	458	1 IF3T_TORCA	P23729 torpedo cal
33	78	6.2	688	1 DNAK_ANAVA	O05714 anabaena va

34 78 6.2 803 1 GYRB_BUCAI P57126 buchnera ap
35 78 6.2 1816 1 KFIB_MOUSE Q60575 mus musculus
36 77.5 6.1 228 1 Z313_MOUSE Q9et26 mus musculus
37 77.5 6.1 640 1 CLAT_MOUSE Q03059 mus musculus
38 77 6.1 249 1 TPIS_TBSPA O83548 treponema p
39 76.5 6.0 455 1 TBA1_SCHPO P04688 schizosacch
40 76 6.0 324 1 NAA2_RHILO Q982f2 rhizobium l
41 76 6.0 385 1 LEF3_NPVAC P41453 autographa
42 76 6.0 820 1 CTNB_TRIGR P32223 tripneustes
43 75.5 6.0 366 1 APN1_YEAST P22936 saccharomyc
44 75.5 6.0 688 1 DNAK_ANASP Q9zej6 anabaena sp
45 75.5 6.0 849 1 AKA4_MOUSE Q60662 mus musculus

ALIGNMENTS

RESULT 1
STC1_HUMAN STANDARD; PRT; 247 AA.
AC P52823;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Stanniocalcin 1 precursor (STC-1).
GN STC1 OR STC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Carnivora; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung carcinoma, and Fibrosarcoma;
RX MEDLINE=96077825; PubMed=7489828;
RA Chang A.C.-M., Janosi J., Hulsbeck M., de Jong D., Jeffrey K.J.,
RA Noble J.R., Reddel R.R.;
RT "A novel human cDNA highly homologous to the fish hormone stanniocalcin";
RL Mol. Cell. Endocrinol. 112:241-247(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal lung;
RX MEDLINE=96312491; PubMed=8700837;
RA Olsen H.S., Cepeda M.A., Zhang Q.-Q., Rosen C.A., Vozzolo B.L.,
RA Wagner G.F.;
RT "Human stanniocalcin: a possible hormonal regulator of mineral metabolism";
RL Proc. Natl. Acad. Sci. U.S.A. 93:1792-1796(1996).
RN [3]
RP SEQUENCE FROM N.A.
RC Jeffrey K.J., Reddel R.R.;
RT "Characterization of the human stanniocalcin 1 gene";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: STIMULATES RENAL PHOSPHATE REABSORPTION, AND COULD THEREFORE PREVENT HYPERCALCEMIA.
CC -!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN MOST TISSUES, WITH THE HIGHEST LEVELS IN OVARY, PROSTATE, HEART, KIDNEY AND THYROID. IN THE KIDNEY, EXPRESSION IS CONFINED TO THE NEPHRON, SPECIFICALLY IN THE DISTAL CONVOLUTED TUBULE AND IN THE COLLECTING TUBULE. NOT DETECTED IN THE BRAIN, LIVER, SPLEEN, PERIPHERAL BLOOD LEUKOCYTES AND ADRENAL MEDULLA.
CC -!- SIMILARITY: BELONGS TO THE STANNIOCALCIN FAMILY.

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DR EMBL; U25997; AAC09472.1; -.
DR EMBL; U46768; AAC88903.1; -.
DR EMBL; AF242179; AAL79522.1; -.
DR Genew; HGNC:11373; STC1.
DR MIM; 601185; -.
DR InterPro; IPR004978; Stanniocalcin.
DR Pfam; PF03298; Stanniocalcin; 1.
KW Hormone; Signal; Glycoprotein.
FT SIGNAL 1 17 POTENTIAL.
FT PROPEP 18 33
FT CHAIN 34 247 STANNIOCALCIN 1.
FT DISULFID 45 59 BY SIMILARITY.
FT DISULFID 54 74 BY SIMILARITY.
FT DISULFID 65 114 BY SIMILARITY.
FT DISULFID 98 128 BY SIMILARITY.
FT DISULFID 135 170 BY SIMILARITY.
FT DISULFID 202 202 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 62 62 N-LINKED (GLCNAC... ) (POTENTIAL).
SQ SEQUENCE 247 AA; 27621 MW; 1E4A8BD861B49AED CRC64;

Query Match 100.0%; Score 1268; DB 1; Length 247;
Best Local Similarity 100.0%; Pred. No. 2.8e-102;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQNSAVLLVLVISASATHEAEQNDVSVPKSRVAAQNSAEVVRCLNSALQVCGCAFACL 60
DB 1 MLQNSAVLLVLVISASATHEAEQNDVSVPKSRVAAQNSAEVVRCLNSALQVCGCAFACL 60
QY 61 ENSTCDTDMYDICKSFYLSAAKFTDQKAFKESLKCIAANGVTSKVFLAIRRCSTFORM 120
DB 61 ENSTCDTDMYDICKSFYLSAAKFTDQKAFKESLKCIAANGVTSKVFLAIRRCSTFORM 120
QY 121 IAEVQECYKLVNCSIAKRNPEAITEVQLPNHFSNRYNRLVRSLLCEDDTVSTIRD 180
DB 121 IAEVQECYKLVNCSIAKRNPEAITEVQLPNHFSNRYNRLVRSLLCEDDTVSTIRD 180
QY 181 SLMEKIGPNMASLPHILOTHCAQTHPRADFNRRRTNEPQKLKVLRLNRGEEDSPSHIK 240
DB 181 SLMEKIGPNMASLPHILOTHCAQTHPRADFNRRRTNEPQKLKVLRLNRGEEDSPSHIK 240
QY 241 RTSHESA 247
DB 241 RTSHESA 247

RESULT 2
STC1_MOUSE STANDARD; PRT; 247 AA.
AC 055183;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Stanniocalcin 1 precursor (STC-1).
GN STC1 OR STC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALE/c;
RX MEDLINE=97179050; PubMed=9027337;
RA Chang A.C.-M., Dunham M.A., Jeffrey K.J., Reddel R.R.;
RT "Molecular cloning and characterization of mouse stanniocalcin cDNA.";
RL Mol. Cell. Endocrinol. 124:185-187(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALE/c;
RX Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: STIMULATES RENAL PHOSPHATE REABSORPTION, AND COULD
CC THEREFORE PREVENT HYPERCALCEMIA (BY SIMILARITY).
CC -!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Secreted.

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CC -!- TISSUE SPECIFICITY: EXPRESSED IN MANY TISSUES.
CC -!- SIMILARITY: BELONGS TO THE STANNIOCALCIN FAMILY.
CC -----
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CC -----
DR EMBL; U47815; AAC00050.1; -.
DR EMBL; BC021425; AAH21425.1; -.
DR MGD; MGI:109131; Stc.
DR InterPro; IPR004978; Stanniocalcin.
DR Pfam; PF03298; Stanniocalcin; 1.
KW Hormone; Signal; Glycoprotein.
FT SIGNAL 1 17 POTENTIAL.
FT PROPEP 18 33
FT CHAIN 34 247 STANNIOCALCIN 1.
FT DISULFID 45 59 BY SIMILARITY.
FT DISULFID 54 74 BY SIMILARITY.
FT DISULFID 65 114 BY SIMILARITY.
FT DISULFID 98 128 BY SIMILARITY.
FT DISULFID 135 170 BY SIMILARITY.
FT DISULFID 202 202 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 62 62 N-LINKED (GLCNAC... ) (POTENTIAL).
SQ SEQUENCE 247 AA; 27480 MW; DAD30D08575A513B CRC64;

Query Match 97.3%; Score 1234; DB 1; Length 247;
Best Local Similarity 96.4%; Pred. No. 2.4e-99;
Matches 238; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 MLQNSAVLLVLVISASATHEAEQNDVSVPKSRVAAQNSAEVVRCLNSALQVCGCAFACL 60
DB 1 MLQNSAVLLVLVISASATHEAEQNDVSVPKSRVAAQNSAEVVRCLNSALQVCGCAFACL 60
QY 61 ENSTCDTDMYDICKSFYLSAAKFTDQKAFKESLKCIAANGVTSKVFLAIRRCSTFORM 120
DB 61 ENSTCDTDMYDICKSFYLSAAKFTDQKAFKESLKCIAANGVTSKVFLAIRRCSTFORM 120
QY 121 IAEVQECYKLVNCSIAKRNPEAITEVQLPNHFSNRYNRLVRSLLCEDDTVSTIRD 180
DB 121 IAEVQECYKLVNCSIAKRNPEAITEVQLPNHFSNRYNRLVRSLLCEDDTVSTIRD 180
QY 181 SLMEKIGPNMASLPHILOTHCAQTHPRADFNRRRTNEPQKLKVLRLNRGEEDSPSHIK 240
DB 181 SLMEKIGPNMASLPHILOTHCAQTHPRADFNRRRTNEPQKLKVLRLNRGEEDSPSHIK 240
QY 241 RTSHESA 247
DB 241 RTSHESA 247

RESULT 3
STC1_RAT STANDARD; PRT; 247 AA.
AC P97574;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Stanniocalcin 1 precursor (STC-1).
GN STC1 OR STC.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Kidney;
RA Abe T., Tanemoto M., Hall A.E., Brown E.M., Hebert S.C.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: STIMULATES RENAL PHOSPHATE REABSORPTION, AND COULD

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CC      THEREFORE PREVENT HYPERCALCEMIA (BY SIMILARITY).
CC      -!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
CC      -!- SUBCELLULAR LOCATION: Secreted.
CC      -!- SIMILARITY: BELONGS TO THE STANNIOCALCIN FAMILY.
CC
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CC      or send an email to license@isb-sib.ch).
CC
CC      EMBL; U62667; AAB39541.1; -.
CC      InterPro; IPR004978; Stanniocalcin.
CC      Pfam; PF03298; Stanniocalcin; 1.
CC      Hormone; Signal; Glycoprotein.
CC      SIGNAL 1 17 POTENTIAL.
CC      PROPEP 18 33 POTENTIAL.
CC      CHAIN 34 247 STANNIOCALCIN 1.
CC      DISULFID 45 59 BY SIMILARITY.
CC      DISULFID 54 74 BY SIMILARITY.
CC      DISULFID 65 114 BY SIMILARITY.
CC      DISULFID 98 128 BY SIMILARITY.
CC      DISULFID 135 170 BY SIMILARITY.
CC      DISULFID 202 202 BY SIMILARITY.
CC      CARBOHYD 62 62 N-LINKED (GLCNAC... ) (POTENTIAL).
CC      SEQUENCE 247 AA; 27507 MW; DAC2FD08575A513B CRC64;
CC
CC      Query Match 97.1%; Score 1231; DB 1; Length 247;
CC      Best Local Similarity 96.0%; Pred. No. 4.3e-99;
CC      Matches 237; Conservative 6; Mismatches 4; Indels 0; Gaps 0;
CC
QY      1 MLQNSAVLLVLVISASATHEAEQNDVSVPKRSRVAQAQNSAEVVRCLNSALQVGCAGFACL 60
DB      1 MLQNSAVLLVLVISASATHEAEQNDVSVPKRSRVAQAQNSAEVVRCLNSALQVGCAGFACL 60
QY      61 ENSTCDTDMGYDICKSFYLSAAKFTQGKAFVKESLKCIAANGVTSKVFLAIRRCSTTFORM 120
DB      61 ENSTCDTDMGYDICKSFYLSAAKFTQGKAFVKESLKCIAANGVTSKVFLAIRRCSTTFORM 120
QY      121 IAEVQEECYKLVNCSIAKRNPEATEVQVLPNHFNSRYNRYNRLVRSLLCEDEDTVSTIRD 180
DB      121 IAEVQEECYKLVNCSIAKRNPEATEVQVLPNHFNSRYNRYNRLVRSLLCEDEDTVSTIRD 180
QY      181 SLMEKIGPNMASLPHILOTDHCAQTHPRADFNRRTNEPQKLKVLRLNRGEGDSPSHIK 240
DB      181 SLMEKIGPNMASLPHILOTDHCAQTHPRADFNRRTNEPQKLKVLRLNRGEGDSPSHIK 240
QY      241 RTSQENA 247
DB      241 RTSQENA 247
CC
CC      RESULT 4
CC      STC_ANGAU STANDARD; PRT; 250 AA.
CC      AC P18301;
CC      DT 01-NOV-1990 (Rel. 16, Created)
CC      DT 15-JUL-1998 (Rel. 36, Last sequence update)
CC      DT 16-OCT-2001 (Rel. 40, Last annotation update)
CC      DE Stanniocalcin precursor (STC) (corpuscles of stannius protein) (CS)
CC      DE (Hypocalcin) (Teleocalcin).
CC      GN STC.
CC      OS Anguilla australis (Australian eel).
CC      OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC      OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguillidae;
CC      OC Anguilla.
CC      OX NCBI_TaxID=7940;
CC      RN [1]
CC      RP SEQUENCE FROM N.A., AND SEQUENCE OF 33-57.
CC      RX MEDLINE=88083961; PubMed=3319739;
CC      RA Butkus A., Roche P.J., Fernley R.T., Haralambidis J.,

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RA      Penchow J.D., Ryan G.B., Trahair J.P., Tregear G.W., Coghlan J.P.;
RT      "Purification and cloning of a corpuscles of Stannius protein from
RT      Anguilla australis.";
RL      Mol. Cell. Endocrinol. 54:123-133(1987).
RN      [2]
RP      REVISIONS.
RA      Roche P.J.;
RL      Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
CC      -!- FUNCTION: ITS PRIMARY FUNCTION IS THE PREVENTION OF HYPERCALCEMIA.
CC      UPON RELEASE INTO THE CIRCULATION, IT LOWERS CALCIUM TRANSPORT BY
CC      THE GILLS, THEREBY REDUCING ITS RATE OF INFUX FROM THE
CC      ENVIRONMENT INTO THE EXTRACELLULAR COMPARTMENT. STC ALSO
CC      STIMULATES PHOSPHATE REABSORPTION BY RENAL PROXIMAL TUBULES. THE
CC      CONSEQUENCE OF THIS ACTION IS INCREASED LEVELS OF PLASMA
CC      PHOSPHATE, WHICH COMBINES WITH EXCESS CALCIUM AND PROMOTES ITS
CC      DISPOSAL INTO BONE AND SCALES.
CC      -!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED.
CC      -!- TISSUE SPECIFICITY: CORPUSCLES OF STANNIUS.
CC      -!- SIMILARITY: BELONGS TO THE STANNIOCALCIN FAMILY.
CC
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CC      or send an email to license@isb-sib.ch).
CC
CC      EMBL; M36967; AAB91483.1; -.
CC      PIR; A54648; A54648.
CC      InterPro; IPR004978; Stanniocalcin.
CC      Pfam; PF03298; Stanniocalcin; 1.
CC      Hormone; Signal; Glycoprotein.
CC      SIGNAL 1 17 POTENTIAL.
CC      PROPEP 18 32 POTENTIAL.
CC      CHAIN 33 250 STANNIOCALCIN.
CC      DISULFID 44 58 BY SIMILARITY.
CC      DISULFID 53 73 BY SIMILARITY.
CC      DISULFID 64 113 BY SIMILARITY.
CC      DISULFID 97 127 BY SIMILARITY.
CC      DISULFID 134 169 BY SIMILARITY.
CC      DISULFID 201 201 INTERCHAIN (BY SIMILARITY).
CC      CARBOHYD 61 61 N-LINKED (GLCNAC... ) (PROBABLE).
CC      SEQUENCE 250 AA; 27174 MW; BB972BD951F75B3E CRC64;
CC
CC      Query Match 53.8%; Score 682; DB 1; Length 250;
CC      Best Local Similarity 54.3%; Pred. No. 8.8e-52;
CC      Matches 138; Conservative 47; Mismatches 57; Indels 12; Gaps 6;
CC
QY      1 MLQNSAVLLVLVISASATHEAEQNDVSVPKRSRVAQAQNSAEVVRCLNSALQVGCAGFACL 60
DB      1 MLQNSAVLLVLVL-VTAAEQDESEPLSPRTARFSASSPSDVARCLNGALQVGCAGFACL 59
QY      61 ENSTCDTDMGYDICKSFYLSAAKFTQGKAFVKESLKCIAANGVTSKVFLAIRRCSTTFORM 120
DB      61 ENSTCDTDMGYDICKSFYLSAAKFTQGKAFVKESLKCIAANGVTSKVFLAIRRCSTTFORM 119
QY      121 IAEVQEECYKLVNCSIAKRNPEATEVQVLPNHFNSRYNRYNRLVRSLLCEDEDTVSTIRD 180
DB      121 IAEVQEECYKLVNCSIAKRNPEATEVQVLPNHFNSRYNRYNRLVRSLLCEDEDTVSTIRD 180
QY      181 SLMEKIGPNMASLPHILOTDHCAQTHPRADFNRRTNEPQKLKVLRLNRGEGDSPSHIK 234
DB      181 SLMEKIGPNMASLPHILOTDHCAQTHPRADFNRRTNEPQKLKVLRLNRGEGDSPSHIK 234
QY      235 SPSTH--KRTSHES 246
DB      238 -PTLFAKKRSTSS 250
CC
CC      RESULT 5
CC      STC_ONCKI STANDARD; PRT; 256 AA.
CC      ID _STC_ONCKI

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Query Match 52.2%, Score 662.5, DB 1; Length 256;
 Best Local Similarity 53.4%; Pred. No. 4.3e-50;
 Matches 125; Conservative 46; Mismatches 54; Indels 9; Gaps 4;

QY 11 LVISASATHEAQNDVSYPKRSRVAQAQNSAEVVRCLNSALOVGCAGFACLENSTCDTDGM 70
 DB 12 LVIGTAATFTDPEEA-SPRRARFSSNSPSDVARCLNGALVGGTTFACLENSTCDTDGM 70
 QY 71 YDICKSFLYSAAKFDTGKAFVKESLRCIANGVTSKVFLAIRRCSFTFMAIEVQEECY 130
 DB 71 HDICQLPFHTAATFTGKTFVKESLRCIANGVTSKVFTIRRCGVQFQMISEVQEECY 130
 QY 131 KLVNCSIAKNPEAITEVWLPNHFNSRYNRLVRSLLCEDEDVTSTIRDSLMKEKIGNM 190
 DB 131 RLDCIGVARSNPEAIGVGVQVPAHFNPRTYSTLLQSLIACDEETVAVVVRAGLVARLPGDM 190
 QY 191 ASLPHILQTDHCAQTHPRADFN-----RRRTNEPQKLKVLRLNLRGEEDSPSHI 239
 DB 191 ETFLQQLLNKHCPQSGNGPSAPAGWRPWPMSPPSKI-QPSWGRD--FTHL 241

RESULT 7

STD_ONCKE	STANDARD;	PRT;	179 AA.
AC	P43647; Q91427;		
DT	01-NOV-1995 (Rel. 32, Created)		
DT	01-NOV-1997 (Rel. 35, Last sequence update)		
DT	16-OCT-2001 (Rel. 40, Last annotation update)		
DE	Stanniocalcin (STC) (Corpuscles of stannius protein) (CS) (Hypocalcin)		
DE	(Teleocalcin).		
GN	STC.		
OS	Oncorhynchus keta (Chum salmon).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei;		
OC	Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.		
OX	NCBI_TaxID=8018;		
RN	[1]		
RP	SEQUENCE FROM N.A., AND SEQUENCE.		
RC	TISSUE=Stannius corpuscles;		
RC	MEDLINE=96077816; PubMed=7489819;		
RA	Yamashita K., Koide Y., Itoh H., Kawada N., Kawachi H.;		
RA	"The complete amino acid sequence of chum salmon stanniocalcin, a		
RT	calcium-regulating hormone in teleosts.";		
RT	Mol. Cell. Endocrinol. 112:159-167(1995).		
RN	[2]		
RP	SEQUENCE OF 1-33.		
RC	TISSUE=Stannius corpuscles;		
RC	MEDLINE=93055697; PubMed=1430418;		
RA	Sundell K., Bjoernsson B.T., Itoh H., Kawachi H.;		
RA	"Chum salmon (Oncorhynchus keta) stanniocalcin inhibits in vitro		
RT	intestinal calcium uptake in Atlantic cod (Gadus morhua).";		
RT	J. Comp. Physiol. B 162:489-495(1992).		
RN	[3]		
RP	DISULFIDE BONDS.		
RP	MEDLINE=99216273; PubMed=10198206;		
RA	Hulova I., Kawachi H.;		
RA	"Assignment of disulfide linkages in chum salmon stanniocalcin.";		
RT	Biochem Biophys. Res. Commun. 257:295-299(1999).		
CC	-1- FUNCTION: ITS PRIMARY FUNCTION IS THE PREVENTION OF HYPERCALCEMIA.		
CC	UPON RELEASE INTO THE CIRCULATION, IT LOWERS CALCIUM TRANSPORT BY		
CC	THE GILLS, THEREBY REDUCING ITS RATE OF INFLUX FROM THE		
CC	ENVIRONMENT INTO THE EXTRACELLULAR COMPARTMENT. STC ALSO		
CC	STIMULATES PHOSPHATE REABSORPTION BY RENAL PROXIMAL TUBULES. THE		
CC	CONSEQUENCE OF THIS ACTION IS INCREASED LEVELS OF PLASMA		
CC	PHOSPHATE, WHICH COMBINES WITH EXCESS CALCIUM AND PROMOTES ITS		
CC	DISPOSAL INTO BONE AND SCALES.		
CC	-1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED.		
CC	-1- SUBCELLULAR LOCATION: Secreted.		
CC	-1- TISSUE SPECIFICITY: PRODUCED AND SECRETED BY THE CORPUSCLES OF		
CC	STANNIUS.		
CC	-1- SIMILARITY: BELONGS TO THE STANNIOCALCIN FAMILY.		

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CC -----
DR EMBL; S80134; AAB35648.2; -
DR InterPro; IPR004978; Stanniocalcin.
DR Pfam; PF03298; Stanniocalcin; 1.
DR Hormone; Glycoprotein; Calcium transport.
FT DISULFID   12      26
FT DISULFID  21    41
FT DISULFID  32    81
FT DISULFID  65    95
FT DISULFID 102   137
FT DISULFID 169   169
FT CARBOHYD  29    29
FT CONFLICT 160   160
FT CONFLICT 170   170
SQ SEQUENCE   179 AA; 19518 MW;  0298CAC33E2B8445 CRC64;
Query Match          48.7%; Score 617; DB 1; Length 179;
Best Local Similarity 66.1%; Pred.No.2.4e-46;
Matches 109; Conservative 28; Mismatches 28; Indels 0; Gaps 0;
QY         40 AEVRLNSALGVGCGAFACLENSTCDTGMVDICKSFLYSAAKFDTOGKAFVKESLKCI 99
DB        :|::|||:|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
       7 SDVAACLNGALDVGGGTFACLENSCTDTGMHDICQLFPHTTAATFNQTGFVKESLRICI 66
QY     100 ANGVTSKVLAIIRCSTFORMIAEOVEECYSKLNVCSIAKRNPPEATTEVVQLPNHFENRY 159
DB        ||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
       67 ANGVTSKVFTIRRCVGFORMISEVQEECYSRLDICGVARSNPPEAIGEVVQPAPHFNNRY 126
QY     160 YNLRVSLLECEDTVSTRISLMKEIGNMASLFPHLOTDHCAQ 204
DB        |:|||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
       127YSTLLQSLLACDEETAVVRAGLVARLGPDMDPFFOLLQNKHCSQ 171

RESULT 8
STC2_MOUSE
ID STC2_MOUSE STANDARD; PRT; 296 AA.
AC O88452;
DT 30-MAY-2000 (Rel. 39, Created)
DD 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Stanniocalcin 2 precursor (STC-2).
GN STC2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Theria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
PI [1]
RNSEQUENCE FROM N.A.
RP MEDLINE=98389283; PubMed=9723890;
RA Chang A.C.-M., Reddel R.R.;
RT "Identification of a second stanniocalcin cDNA in mouse and human:
RStanniocalcin 2."
RL Mol. Cell. Endocrinol. 141:95-99(1998).
[2]
RNSEQUENCE FROM N.A., AND CHARACTERIZATION.
RP TISSUE=Breast carcinoma;
RX MEDLINE=99378040; PubMed=10450831;
RA Moore E.E., Kuestner R.E., Conklin D.C., Whitmore T.E., Downey W.,
RA Buddle M.M., Adams R.L., Bell L.A., Thompson D.B., Wolf A., Chen L.,
RA Stamm M.R., Grant F.J., Lok S., Ren H., de Jongh K.S.;
RT "Stanniocalcin 2: characterization of the protein and its localization
Rto human pancreatic alpha cells."
RL Horm. Metab. Res. 31:406-414(1999).
[3]
RNSEQUENCE FROM N.A.
RP TISSUE=Breast tumor;
RX Strausberg R.
```

TISSUE=Breast tumor;
Strausberg R.;

Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: HAS AN ANTI-HYPOCALCEMIC ACTION ON CALCIUM AND PHOSPHATE
 CC HOMEOSTASIS.
 CC -!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Secreted (Potential).
 CC -!- TISSUE SPECIFICITY: FOUND IN A VARIETY OF TISSUES INCLUDING
 CC SKELETAL MUSCLE, SMALL INTESTINE, KIDNEY, LIVER AND BRAIN.
 CC -!- SIMILARITY: BELONGS TO THE STANNIOCALCIN FAMILY.
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 CC
 DR EMBL; AF056244; AAC27507.1; -;
 DR EMBL; AF031035; AAD01921.1; -;
 DR EMBL; BC012206; AAH12206.1; -;
 DR MGD; MGI:1316731; Stc2.
 DR InterPro: IPR004978; Stannioalcin.
 DR Pfam; PF03298; Stannioalcin; 1.
 KW Hormone; Signal; Glycoprotein.
 FT SIGNAL 1 24 POTENTIAL.
 FT CHAIN 25 296 STANNIOCALCIN 2.
 FT CARBOHYD 73 73 N-LINKED (GLCNAC...) (POTENTIAL).
 FT SEQUENCE 296 AA; 32601 MW; 0CIEF4008912DE68 CRC64;
 SQ
 Query Match 28.0%; Score 354.5; DB 1; Length 296;
 Best Local Similarity 31.7%; Pred. No. 1.8e-23;
 Matches 85; Conservative 45; Mismatches 109; Indels 29; Gaps 5;
 QY 7 VLLVIVISASATHEAFQNDVSP-----RKSRAVAQNSAEVRCVCLNSALQVCGCA 56
 DB 10 VTALVLF--ATLDPAQGTDTSTNPPEGPDRSSQKGRSLQNTAIOHCLVNAVGVCGV 67
 QY 57 FACLENSTCDTDMGYDICKSFLYSAAKPTQKAFVKESLKCIANGVTSKVELAIRRCST 116
 DB 68 FCFENNSEIOGLHGICMTFLHNAKGFDAQKSFIKDALKRCAHALHKFCISRKCPA 127
 QY 117 FORMIAEQEYKSLNVCSIAKRNPEATEVTVQVLPNHFNSRYNRLVRSLLCEDDTVS 176
 DB 128 IREMFVQLQRECYLKHDLCSAQENVGVIVEMIFHKOLLHPYVDLVNLLITCGEDVKE 187
 QY 177 TIRDSLMKXIGPNWASLFHIL-----QTDHCAQTH-----PRADFNRERRNEPQKLKV 224
 DB 188 AVTRSVQAQCEQSGWGLCSILSFCTSNIQRPPTAAPEHQPLADRAQLGRPHRDTDHHLT 247
 QY 225 LLRLNRGEDSPSHIK-----RTSHESA 247
 DB 248 ANRGAKGERGSKSHPNAHARGTGGQSA 275
 ID STC2 HUMAN STANDARD; PRT; 302 AA.
 AC O76061.
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Stannioalcin 2 precursor (STC-2) (Stannioalcin-related protein)
 DE (STCRP) (STC-related protein).
 GN STC2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98389283; PubMed=9723890;
 RA Chang A.C.-W., Reddel R.R.;
 RT "Identification of a second stannioalcin cDNA in mouse and human:

stannioalcin 2.";
 RL Mol. Cell. Endocrinol. 141:95-99 (1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Osteosarcoma;
 RX MEDLINE=98440784; PubMed=9753616;
 RA Ishiabashi K., Miyamoto K., Taketani Y., Morita K., Takeda E.,
 RA Sasaki S., Inai M.;
 RT "Molecular cloning of a second human stannioalcin homologue (STC2).";
 RL Biochem. Biophys. Res. Commun. 250:252-258 (1998).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99145369; PubMed=10022771;
 RA DiMattia G.E., Varghese R., Wagner G.F.;
 RT "Molecular cloning and characterization of stannioalcin-related
 RT protein.";
 RL Mol. Cell. Endocrinol. 146:137-140 (1998).
 RN [4]
 RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
 RC TISSUE=Breast Carcinoma;
 RX MEDLINE=99378040; PubMed=10450831;
 RA Moore E.E., Kuestner R.E., Conklin D.C., Whitmore T.E., Downey W.,
 RA Buddle M.W., Adams R.L., Bell L.A., Thompson D.L., Wolf A., Chen L.,
 RA Stamm M.R., Grant F.J., Lok S., Ren H., de Jongh K.S.;
 RT "Stannioalcin 2: characterization of the protein and its localization
 RT to human pancreatic alpha cells.";
 RL Horm. Metab. Res. 31:406-414 (1999).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney, and Muscle;
 RA Strausberg R.;
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: HAS AN ANTI-HYPOCALCEMIC ACTION ON CALCIUM AND PHOSPHATE
 CC HOMEOSTASIS.
 CC -!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED.
 CC -!- SUBCELLULAR LOCATION: Secreted (Potential).
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN A VARIETY OF TISSUES INCLUDING
 CC MUSCLE, HEART, PANCREAS, KIDNEY, SPLEEN, PROSTATE, SMALL
 CC INTESTINE, COLON AND PERIPHERAL BLOOD LEUCOCYTES.
 CC -!- SIMILARITY: BELONGS TO THE STANNIOCALCIN FAMILY.
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 DR EMBL; AF055460; AAC27036.1; -;
 DR EMBL; AB012664; BAA33489.1; -;
 DR EMBL; AF098452; AAC97948.1; -;
 DR EMBL; AF031036; AAD01922.1; -;
 DR EMBL; BC000658; AAH00658.1; -;
 DR EMBL; BC006352; AAH06352.1; -;
 DR EMBL; BC013958; AAH13958.1; -;
 DR Genew; HGNC:11374; STC2.
 DR MIM; 603665; -;
 DR InterPro: IPR004978; Stannioalcin.
 DR Pfam; PF03298; Stannioalcin; 1.
 KW Hormone; Signal; Glycoprotein.
 FT SIGNAL 1 24 POTENTIAL.
 FT CHAIN 25 302 STANNIOCALCIN 2.
 FT CARBOHYD 73 73 N-LINKED (GLCNAC...) (POTENTIAL).
 FT SEQUENCE 302 AA; 33248 MW; 9B90D8911524FA22 CRC64;
 SQ
 Query Match 27.9%; Score 354; DB 1; Length 302;
 Best Local Similarity 32.4%; Pred. No. 2e-23;
 Matches 83; Conservative 45; Mismatches 102; Indels 26; Gaps 4;
 QY 9 LVLVVIS-----ASATHEAF-QNDSVSPKRSRAVAQNSAEVRCVCLNSALQVCGCA 60
 DB 12 LALVLATFDPAFGTDTATNPPEGPDRSSQKGRSLQNTAIOHCLVNAVGVCGVCF 71

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QY 61 ENSTCDTDMYDICKSFLYSAAKFTQKAFVKESLKCIANGVTGKVFIAIRRCSTFORM 120
Db 72 ENNSCEIRGLHIGICMTFLHNAGKFAQKSFIDKALKCKAHALRHRFGCISRKCPAIREM 131
QY 121 IAEVQEECYKLVNCSIAKRNPEATEVVQLPNHFSNRYNRLVRSLLCEDEDTVTIRD 180
Db 132 VQORECYLKHDLCAAQENTRIVEMHFKDLLLHPEYVDVNLTLTCGEEVKEATH 191
QY 181 SLMEKIGPNMASHILO-TDCAOTHPRADFNRRRTNEPKL----- 222
Db 192 SVQVQCEQNWGSLCSILSFTSAIQPPTAPPERQPOVDRTKLSRAHHGEAGHLPSPS 251
QY 223 KVLNLRGEEDESPSH 238
Db 252 RETGRGAKGERGSKSH 267

RESULT 10
STC2 MACNE STANDARD; PRT; 302 AA.
AC O97561;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Stanniocalcin 2 precursor (STC-2).
GN STC2.
OS Macaca nemestrina (Pig-tailed macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
OX NCBI_TaxID=9545;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=99378040; PubMed=10450831;
RX Moore E.E., Kuestner R.E., Conklin D.C., Whitmore T.E., Downey W.,
RA Buddle M.R., Adams R.L., Bell L.A., Thompson D.L., Wolf A., Chen L.,
RA Stamm M.R., Grant F.J., Lok S., Ren H., de Jongh K.S.;
RT "Stanniocalcin 2: characterization of the protein and its localization
to human pancreatic alpha cells.";
RL Horm. Metab. Res. 31:406-414(1999).
CC CC
CC -!- FUNCTION: HAS AN ANTI-HYPOCALCEMIC ACTION ON CALCIUM AND PHOSPHATE
HOMEOSTASIS.
CC -!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Secreted (Potential).
CC -!- SIMILARITY: BELONGS TO THE STANNIOCALCIN FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
DR EMBL; AF035377; AAD0207.1; -.
DR InterPro; IPR004978; Stanniocalcin.
DR Pfam; PF03298; Stanniocalcin; 1.
KW Hormone; Signal; Glycoprotein.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 302 STANNIOCALCIN 2.
FT CARBOHYD 73 73 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 302 AA; 33281 MW; 62953CE95AF64C1 CRC64;

Query Match 27.8%; Score 352; DB 1; Length 302;
Best Local Similarity 32.8%; Pred. No. 3e-23;
Matches 84; Conservative 44; Mismatches 102; Indels 26; Gaps 5;

QY 9 LVLVIS-----ASATHEAE-QNDSVSPKSRVAQAQNSAEVVRCLNSALQVCGGAFACL 60
Db 12 LALVLATIDPARGTDATNPPEGQDRSSQOKGRSLQNTAEIOHCLVNLNAGDVCGVFCF 71

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QY 61 ENSTCDTDMYDICKSFLYSAAKFTQKAFVKESLKCIANGVTGKVFIAIRRCSTFORM 120
Db 72 ENNSCEIRGLHIGICMTFLHNAGKFAQKSFIDKALKCKAHALRHRFGCISRKCPAIREM 131
QY 121 IAEVQEECYKLVNCSIAKRNPEATEVVQLPNHFSNRYNRLVRSLLCEDEDTVTIRD 180
Db 132 VQORECYLKHDLCAAQENTRIVEMHFKDLLLHPEYVDVNLTLTCGEEVKEATH 191
QY 181 SLMEKIGPNMASHILO-TDCAOTHPRADFNRRRTNEPKL----- 222
Db 192 SVQVQCEQNWGSLCSILSFTSAIQPPTAPPERQPOVDRTKLSRAHHGEAGHLPSPS 251
QY 223 KVLNLRGEEDESPSH 238
Db 252 RETGRGAKGERGSKSH 267

RESULT 11
STC2 RAT STANDARD; PRT; 296 AA.
AC Q9ROK8;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Stanniocalcin 2 precursor (STC-2).
GN STC2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=99439722; PubMed=10508929;
RA Honda S., Kashiwagi M., Okata K., Tojo A., Hirose S.;
RT "Regulation by alpha,25-dihydroxyvitamin D(3) of expression of
stanniocalcin messages in the rat kidney and ovary.";
RL FEBS Lett. 459:119-122(1999).
CC CC
CC -!- FUNCTION: HAS AN ANTI-HYPOCALCEMIC ACTION ON CALCIUM AND PHOSPHATE
HOMEOSTASIS.
CC -!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Secreted (Potential).
CC -!- TISSUE SPECIFICITY: EXPRESSED IN A VARIETY OF TISSUES. STRONGLY
EXPRESSED IN OVARY AND TO A LESSER EXTENT IN KIDNEY.
CC -!- SIMILARITY: BELONGS TO THE STANNIOCALCIN FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AB030707; BAA85251.1; -.
DR InterPro; IPR004978; Stanniocalcin.
DR Pfam; PF03298; Stanniocalcin; 1.
KW Hormone; Signal; Glycoprotein.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 296 STANNIOCALCIN 2.
FT CARBOHYD 73 73 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 296 AA; 32621 MW; 0903639858D9B2DC CRC64;

Query Match 27.5%; Score 349; DB 1; Length 296;
Best Local Similarity 31.8%; Pred. No. 5.3e-23;
Matches 81; Conservative 44; Mismatches 106; Indels 24; Gaps 4;

QY 7 VLLVLVISASATHAEQNDQSVSP-----RKSRVAQAQNSAEVVRCLNSALQVCGCA 56
Db 10 VTLALVF--ATLDPARGTDTNPPGPDGRSSQOKGRSLQNTAEIOHCLVNLNAGDVCGV 67
QY 57 FACLENSTCDTDMYDICKSFLYSAAKFTQKAFVKESLKCIANGVTGKVFIAIRRCST 116

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Db 68 FECFENNCEIOGLHGICMTFLHNAKGFDAQKGFIFKDALRCVAHALRHKFCISRKCPA 127
QY 117 FORMIAEVEQECYKLVNCSIAKRNPEALTEVVQLPNHFNSRYNRLVRSLLCEDEDTVS 176
Db 128 IREMYVQLORECYKLDLCSAQENVVIVEMHFKDLLLHFPYVDLVNLLTTCGEDVRE 187
QY 177 TTRDSLMKEIGPNMASLFHL-----OTDHCQATH-----PRADFNRRTNFEQKLKV 224
Db 188 AVTRSVQAQCEQSGWGLCSILSFCTSNIQRPPTAAPEHQPLADRAQLSRPYHRTDHHLT 247
QY 225 LLRNLRGEEDSPSHI 239
Db 248 ANRGKGERGSKSHL 262

RESULT 12
STC2_CAVPO
ID STC2_CAVPO STANDARD; PRT; 197 AA.
AC P57675;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Stanniocalcin 2 (STC-2) (Fragments).
GN STC2.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE.
RX MEDLINE=99378040; PubMed=10450831;
RA Moore E.E., Kuestner R.E., Conklin D.C., Whitmore T.E., Downey W.,
RA Buddle M.M., Adams R.L., Bell L.A., Thompson D.L., Wolf A., Chen L.,
RA Stamm M.R., Grant F.J., Lok S., Ren H., de Jongh K.S.;
RT "Stanniocalcin 2: characterization of the protein and its localization
RT to human pancreatic alpha cells."
RL Horm. Metab. Res. 31:406-414(1999).
CC -!- FUNCTION: HAS AN ANTI-HYPOCALCEMIC ACTION ON CALCIUM AND PHOSPHATE
CC HOMEOSTASIS.
CC -!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Secreted (Potential).
CC -!- SIMILARITY: BELONGS TO THE STANNIOCALCIN FAMILY.
KW Hormone.
FT NON_CONS 60 61
FT NON_CONS 64 65
FT NON_CONS 69 70
FT NON_CONS 75 76
FT NON_CONS 92 93
FT NON_CONS 154 155
SQ SEQUENCE 197 AA; 21899 MW; 1512DAB59C8A8E67 CRC64;

Query Match 14.3%; Score 181.5; DB 1; Length 197;
Best Local Similarity 25.8%; Pred. No. 8.8e-09;
Matches 58; Conservative 27; Mismatches 85; Indels 55; Gaps 6;

QY 25 DSVSPKSRVAAQNSAEVVRCLNSALQVCGGAFACLENSTCDTDGMVDICKSFLYSAAKF 84
Db 12 DRGSOQKGLSLQNTAEIQHCLVNAQDVGCGVFECFENNXCIXLHXI----- 60
QY 85 DTQGAFFVESLUCIKANGVTSKVFIAIRCSTFORMIAEVBQECYKLVNCSIAKRNPEA 144
Db 61 -----SFIAKH-----ALRFGCISREMVQLORECYKLDKLCMINFR----- 97
QY 145 ITEVVQLPNHFNRYNRLVRSLLCEDEDTVSTIRDSLMKEIGPNMASLFHL-----QT 199
Db 98 -----DLLLHFPYVDLVNLLTTCGEDVKAATRSIQAQEQNWGLCSILSFCTSNV 149
QY 200 DHCAQTHPRADFNRRRTNEP-----QKLKVLRLNRGEEDSPSH 238
Db 150 QRPXAXQPKAD--RAQVSRPHHDTGHHLLLEAIXGKGERGSKSH 192

RESULT 13

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STC_ONCNE
ID STC_ONCNE STANDARD; PRT; 40 AA.
AC P43649;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Stanniocalcin (STC) (Corpuscles of stannius protein) (CS) (Hypocalcin)
DE (Teleocalcin) (Fragment).
GN STC.
OS Oncorhynchus nerka (Sockeye salmon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8023;
RN [1]
RP SEQUENCE.
RX MEDLINE=89065334; PubMed=3197944;
RA Wagner G.F., Fenwick J.C., Park C.M., Milliken C., Copp D.H.,
RA Friesen H.G.;
RT "Comparative biochemistry and physiology of teleocalcin from sockeye
RT and coho salmon."
RL Gen. Comp. Endocrinol. 72:237-246(1988).
CC -!- FUNCTION: ITS PRIMARY FUNCTION IS THE PREVENTION OF HYPERCALCEMIA.
CC UPON RELEASE INTO THE CIRCULATION, IT LOWERS CALCIUM TRANSPORT BY
CC THE GILLS, THEREBY REDUCING ITS RATE OF INFLUX FROM THE
CC ENVIRONMENT INTO THE EXTRACELLULAR COMPARTMENT. STC ALSO
CC STIMULATES PHOSPHATE REABSORPTION BY RENAL PROXIMAL TUBULES. THE
CC CONSEQUENCE OF THIS ACTION IS INCREASED LEVELS OF PLASMA
CC PHOSPHATE, WHICH COMBINES WITH EXCESS CALCIUM AND PROMOTES ITS
CC DISPOSAL INTO BONE AND SCALES.
CC -!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: PRODUCED AND SECRETED BY THE CORPUSCLES OF
CC STANNIUS.
CC -!- SIMILARITY: BELONGS TO THE STANNIOCALCIN FAMILY.
DR PIR; A60841;
DR InterPro; IPR004978; Stanniocalcin.
KW Pfam; PF03298; Stanniocalcin; 1.
KW Hormone; Glycoprotein; Calcium transport.
FT CARBOHYD 29 29 N-LINKED (GLCNAC. . .).
FT UNSURE 29 29
FT NON_TER 40 40
SQ SEQUENCE 40 AA; 4134 MW; 0C517B7BBBC5EB6C CRC64;

Query Match 12.3%; Score 156; DB 1; Length 40;
Best Local Similarity 79.4%; Pred. No. 2.1e-07;
Matches 27; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 40 AEVVRCLNSALQVCGGAFACLENSTCDTDGMVDI 73
Db 7 SDVARCLNGALDVCGGTACLENSTCDTDGMWDI 40

RESULT 14
A3B1_MOUSE
ID A3B1_MOUSE STANDARD; PRT; 1105 AA.
AC Q921T1;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Adapter-related protein complex 3 beta 1 subunit (Beta-adaptin 3A)
DE (AP-3 complex beta-3A subunit) (Beta-3A-adaptin).
GN AP3B1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/HeJ;
RX MEDLINE=99135912; PubMed=9931340;
RA Feng L., Seymouar A.B., Jiang S.Y., To A., Peden A.A., Novak E.K.,
RA Zhen L., Rusiniak M.E., Bicher E.M., Robinson M.S., Gorin M.B.,

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OM protein - protein search, using sw model

Run on: June 12, 2003, 19:05:48 ; Search time 59 Seconds
(without alignments)
862.604 Million cell updates/sec

Title: US-09-705-500A-3
Perfect score: 1268
Sequence: 1 MLQNSAVLLVLVISASATHE.....NLRGEDSPSHIKRTSHESA 247

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL 21.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phase.*
10: sp_plant.*
11: sp_rhodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_rvirus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1199	94.6	247	6 Q9N0T1	Q9n0t1 bos taurus
2	654	51.6	249	13 Q98T57	Q98tb7 osteoglossu
3	354.5	28.0	296	11 Q9DCS6	Q9dcs6 mus musculu
4	102	8.0	473	10 Q9SZ16	Q9sz16 arabidopsis
5	92	7.3	1108	11 Q91YR4	Q91yr4 mus musculu
6	90.5	7.1	454	5 Q9GV74	Q9gv74 dictyosteli
7	90.5	7.1	783	3 O14130	O14130 schizosacch
8	89.5	7.1	1126	10 O64605	O64605 arabidopsis
9	89.5	7.1	3658	10 Q9M7K6	Q9m7k6 arabidopsis
10	89	7.0	305	10 O65029	O65029 linum usita
11	89	7.0	1728	10 Q9LUI2	Q9lui2 arabidopsis
12	88	6.9	473	10 Q9LFC2	Q9lfc2 arabidopsis
13	87	6.9	284	10 Q8VY30	Q8vy30 arabidopsis
14	86	6.8	470	16 Q9Z8Q2	Q9z8q2 chlamydia p
15	86	6.8	510	10 Q9LFC4	Q9lfc4 arabidopsis
16	86	6.8	556	3 Q03899	Q03899 saccharomyc

17	85.5	6.7	290	10 Q948Q0	Q948q0 hevea bras
18	85.5	6.7	634	5 Q95PL8	Q95pl8 trypanosoma
19	85	6.7	806	10 Q9FFZ5	Q9ffz5 arabidopsis
20	83.5	6.6	427	5 Q9N3E2	Q9n3e2 caenorhabdi
21	83.5	6.6	1026	3 Q74669	Q74669 pneumocysti
22	83.5	6.6	1028	3 Q74668	Q74668 pneumocysti
23	83.5	6.6	1273	5 Q9BL02	Q9bl02 caenorhabdi
24	83	6.5	250	17 Q04927	Q04927 methanobact
25	83	6.5	297	12 Q91BU2	Q91bj2 spodoptera
26	83	6.5	365	10 Q9SU53	Q9su53 arabidopsis
27	83	6.5	848	6 Q9XS94	Q9xs94 bos taurus
28	82.5	6.5	869	5 Q94174	Q94174 caenorhabdi
29	82.5	6.5	1757	10 Q9SMY5	Q9sm5 arabidopsis
30	82.5	6.5	2335	3 O14356	O14356 schizosacch
31	82.5	6.5	2535	10 Q9SZ40	Q9sz40 arabidopsis
32	82	6.5	329	12 Q9PYT2	Q9pyt2 xestia c-ni
33	82	6.5	453	2 Q8QWV5	Q8qvw5 lactobacill
34	82	6.5	815	16 Q9X2B4	Q9x2b4 thermotoga
35	82	6.5	925	10 Q9ZTA5	Q9zta5 arabidopsis
36	81.5	6.4	189	10 Q8VWM1	Q8vwm1 gossypium h
37	81.5	6.4	463	5 Q17665	Q17665 caenorhabdi
38	81.5	6.4	549	16 O25619	O25619 helicobacte
39	81.5	6.4	757	4 Q8TAG9	Q8tag9 homo sapien
40	81.5	6.4	826	12 Q9PZ22	Q9pzz2 xestia c-ni
41	81.5	6.4	974	10 Q9FIT7	Q9fic7 arabidopsis
42	81.5	6.4	974	10 Q94BP1	Q94bp1 arabidopsis
43	81.5	6.4	2931	5 Q9W2C6	Q9w2c6 drosophila
44	81	6.4	332	2 Q59904	Q59904 serratia en
45	81	6.4	358	16 Q55875	Q55875 synechocyst

ALIGNMENTS

RESULT 1

ID Q9N0T1 PRELIMINARY; PRT; 247 AA.
AC Q9N0T1;
DT 01-OCT-2000 (TremBLrel. 15, Created)
DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TremBLrel. 21, Last annotation update)
DE Stanniocalcin.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_taxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=OVARY;
RA DiMattia G.E.;
RT "bovine stanniocalcin cDNA sequence."
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF257506; AAF68996.1; -;
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR004978; Stanniocalcin.
DR Pfam; PF03298; Stanniocalcin; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; UNKNOWN 1.
SQ SEQUENCE 247 AA; 27555 MW; F9942A715E2A3D0 CRC64;

Query Match 94.6%; Score 1199; DB 6; Length 247;
Best Local Similarity 94.7%; Pred. No. 2.2e-106;
Matches 234; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

Qy	1	MLQNSAVLLVLVISASATHEAQNDSVSPKRSRVAQAQNSAEVRLNSALQVGCAGACL	60
Db	1	MLQNSAVLLVLVISASATHEAQNDSVSPKRSRVAQAQNSAEVRLNSALQVGCAGACL	60
Qy	61	ENSTCDTDGMYDICKSFYLSAAKFDTCQKAFVKESLKCIAANGVTSKVFLAIRRCSSTFORM	120
Db	61	ENSTCDTDGMYDICKSFYLSAAKFDTCQKAFVKESLKCIAANGVTSKVFLAIRRCSSTFORM	120
Qy	121	IAEQEECYSKLVNCSIAKRNPFAITEYVOLPNHFSNRYNRLVRSLLCEDDTVSTIRD	180

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Db 121 IAEVQECYKLVNCSVAKRNPETAEVQVLPNHFNRNRYNRLVRSLLDCDDTSTIRD 180
Qy 181 SLMEKIGPNMNSLPHILOTDHCAQTHPRADFNRRRTNEPQKLVLLRNLRGEEDSPSHIK 240
Db 181 SLMEKIGPNMNSLPHILOTDHCAQTHPRADFNRRRTNEPQKLVLLRNLRGEEDSPSHIK 240
Qy 241 RTSHESA 247
Db 241 RTSQESA 247

RESULT 2
Q98TB7 PRELIMINARY; PRT; 249 AA.
AC Q98TB7;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Stanniocalcin precursor.
GN STC.
OS Osteoglossum bicirrhosum (silver arawana).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteoglossomorpha;
OC Osteoglossiformes; Osteoglossidae; Osteoglossum.
OX NCBI_TaxID=109271;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=CORPUSCLE OF STANNIUS;
RA Amemiya Y., Marra L.E., Reyhani N., Youson J.H.;
RT "Stanniocalcin from an ancient teleost. Evidence for a monomeric form
of the hormone and an extracorporeal distribution.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB060558; BAB43868.1; --
DR InterPro; IPR004978; Stanniocalcin.
DR Pfam; PF03298; Stanniocalcin; 1.
KW Signal.
FT SIGNAL 1 31 POTENTIAL.
FT CHAIN 32 249 POTENTIAL.
SQ SEQUENCE 249 AA; 27389 MW; 10297D0542BEB3A CRC64;

Query Match 51.6%; Score 654; DB 13; Length 249;
Best Local Similarity 57.5%; Pred. No. 2.2e-54;
Matches 122; Conservative 43; Mismatches 45; Indels 2; Gaps 1;

Qy 1 MLONSAVLLVVISASATHEAEQNDSVSPKRSRVAQNSAEVVRCLNSALQVGCAPACL 60
Db 1 MIQKCMVLLLFLLTASAP--VIDQEPSPTRTARFAANSLSDVARCLSGALQVGCAPACL 58
Qy 61 ENSTCDDTGMVDYICKSFYSAKFTDTQKAFVKESLKCANGVTSKVFLAIRRCSTFORM 120
Db 59 ENSTCDDTGMVEICKFTLYTAAKFTDTQKTFVKESLRCWANGITSGFLMVRRCSTFORM 118
Qy 121 IAEVQECYKLVNCSIAKRNPEAITEVQVLPNHFNRNRYNRLVRSLLDCDDTSTIRD 180
Db 119 LADVQEDCVNKLDCGVARANPEAIGEAQLPNSFPNRHYSFLQLSLLCEQDETSLYRD 178
Qy 181 SLMEKIGPNMNSLPHILOTDHCAQTHPRADFN 212
Db 179 SMSARLGPEVAMLFKLQSSRSRSGAAQASNN 210

RESULT 3
Q9DCS6 PRELIMINARY; PRT; 296 AA.
AC Q9DCS6;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Stanniocalcin 2.
GN STC2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=KIDNEY;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yananaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tonita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Yushwa-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RT Hayashizaki Y.;
RL "Functional annotation of a full-length mouse cDNA collection.";
DR EMBL; AK002527; BAB22164.1; --
DR MGD; MGI:1316731; Stc2.
DR InterPro; IPR004978; Stanniocalcin.
DR Pfam; PF03298; Stanniocalcin; 1.
SQ SEQUENCE 296 AA; 32488 MW; BD8961CEFFA47508 CRC64;

Query Match 28.0%; Score 354.5; DB 11; Length 296;
Best Local Similarity 31.7%; Pred. No. 1e-25;
Matches 85; Conservative 45; Mismatches 109; Indels 29; Gaps 5;

Qy 7 VLLVLVISASATHEAEQNDSVSP-----RKSRVAQNSAEVVRCLNSALQVGCGA 56
Db 10 VTLALVP--ATLDPAQGTDTNPPGQDRSSQKGLSLQNTAEIQLCLNAGDVGCV 67
Qy 57 FACLENSTCDDTGMVDYICKSFYSAKFTDTQKAFVKESLKCANGVTSKVFLAIRRCST 116
Db 68 PECFENNSCETQGLGHICMTFLNAGKFDQKGFIDALCKAHLAKHFKGICSRKCPA 127
Qy 117 FORMIAEVEECYKLVNCSIAKRNPEAITEVQVLPNHFNRNRYNRLVRSLLCEQDVTVS 176
Db 128 IRENVFQVQRECYLKHDLCLCSAAQENVGIVEMIHFKDLLLHEPYVDLVNLLLTGCEVKE 187
Qy 177 TIRDSLMEKIGPNMNSLPHIL-----QTDHCAQTH-----PRADFNRRRTNEPQKLV 224
Db 188 AVTRSVQAQCEQSGGLCSILSFCTSNIQRPPTAAPHQPLADRAQLSRPHHRTDHHLT 247
Qy 225 LLRNLRGEEDSPSHIK-----RTSHESA 247
Db 248 ANRGAKGERGSKSHPNAHARGRTGQSA 275

RESULT 4
Q9SZ16 PRELIMINARY; PRT; 473 AA.
AC Q9SZ16;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE Hypothetical 53.7 kDa protein.
GN F10W23.100 OR At4G26760.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OX eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.

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QY 61 ENSTCDDTGMWD-ICKSFLYSAAKFDTGKAFVKESKCIANGVTSKVF----- 101
 Db 358 ATMSIERKGMPEPYLKSF-YVRSSTDPTMIKTLKLEILTNLNLANEANTLLRFEQTYVRSQ 416
 QY 110 -----AIRCSIFORMIAEQEVCYKLVNCSIARNPEAITE---VVOLPNHFS 156
 Db 417 DKQFAAANTIQIGCAT---SISVTTCTLNGL-VCLLSNRDEIVVAESVVVKKLLQMQ 472
 QY 157 NRYYNRLVRSLE-CDEDTVSTIRDSLMEKIGPNMASLPHILOTHCAQTHPRADFNRR 215
 Db 473 PAQHGEIIRHMAKLLDSITPVARASILWILIGEN-----CERVPKIA----- 514
 QY 216 TNEPOKLVLLNLRGSED 234
 Db 515 ---PDVLRKMAKSFSEDD 530
 RESULT 6
 Q9GV74
 ID Q9GV74 PRELIMINARY; PRT; 454 AA.
 AC Q9GV74;
 DT 01-MAR-2001 (TRENBLrel. 16, Created)
 DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TRENBLrel. 16, Last annotation update)
 DE Differentiation associate-1.
 GN DIA-1.
 OS Dictyostelium discoideum (Slime mold).
 OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
 OX NCBI_TaxID=44689;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20347020; PubMed=10887082;
 RA Hirose S., Inazu Y., Chae S., Maeda Y.;
 RT "Suppression of the growth/differentiation transition in Dictyostelium
 RL development by transient expression of a novel gene, dial.";
 RL Development 127:3263-3270(2000).
 DR EMBL; AB007026; BAB13513.; -.
 SQ SEQUENCE 454 AA; 48601 MW; 529D28B2D1908B95 CRC64;
 Query Match 7.1%; Score 90.5; DB 5; Length 454;
 Best Local Similarity 21.1%; Pred No.2.7;
 Matches 46; Conservative 42; Mismatches 93; Indels 37; Gaps 11
 QY 45 CLNSALQVCGGAFACLENSTCDTGMVDICKSFLYSAAKFDTGK----AFVKESLKCIA 100
 Db 227 CLNGANGYSKSY--VENQSCDPSDEYPCVNSD-YQCKCNCKGKGCQSYKKLTQEC-- 281
 QY 101 NGVTSKVFATRCSTFORMIAE-----VOEVCYKLVNCSIARNPEAITEVVQLPNHF 155
 Db 282 KDSSNKLVL----CAKSKNGIPSYKDYVTQTNCOSQL--CNYSR---DCIDPKAKVSTCF 332
 QY 156 SN-----RYYNRLVRSILLECDTGVSTIRDSLMEKIGPNMASLPHILOTHCAQTHPRA 209
 Db 333 NDLFLMCPRYQPEIEGSS 391
 QY 210 DFNRRRTNEPOKLVLLNLRGSEDSPSHIKRTSHESA 247
 Db 392 NSVSSESSSPSSSV-----ESSNSKSNHTSSSS 422
 RESULT 7
 O14130
 ID O14130 PRELIMINARY; PRT; 783 AA.
 AC O14130;
 DT 01-JAN-1999 (TRENBLrel. 09, Created)
 DT 01-JAN-1999 (TRENBLrel. 09, Last sequence update)
 DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)
 DE Putative 88.0 kDa transcriptional regulatory protein C3C7.04 in
 GN chromosome I.
 GN SPAC3C7.04.
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetaceae;

OC Schizosaccharomyces.
 RN NCBI_TaxID=4896;
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RA Brown D., Churher C.M., Wood V., Barrell B.G., Rajandream M.A.;
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
 RR -!- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
 CC -!- SIMILARITY: CONTAINS A ZN(2)-CYS(6), FUNGAL-TYPE BINUCLEAR CLUSTER
 DOMAIN
 CC EMBL; Z9568; CAB16735.1; -.
 DR HSSP; P12351; 1HWT.
 DR InterPro; IPR002106; AALRNA ligaseII.
 DR InterPro; IPR001138; Fungi_Trn.
 DR Pfam; PF00172; Zn.clus; 1.
 DR SMART; SM00066; GAL4.1.
 DR PROSITE; PS00339; AA_TRNA_LIGASE_II_2; UNKNOWN_1.
 DR PROSITE; PS00463; ZN2_CYS6_FUNGAL_1.
 DR PROSITE; PS00468; ZN2_CYS6_FUNGAL_2; 1.
 KW Hypothetical protein; Transcription regulation; DNA-binding;
 KW Nuclear protein; Zinc; Metal-binding; Transmembrane.
 FT DNA_BIND 40 66 ZN(2)-CYS(6), FUNGAL-TYPE.
 FT DOMAIN 24 27 POLY-ARG.
 FT DOMAIN 32 35 POLY-ARG.
 FT DOMAIN 276 279 POLY-PHE.
 FT TRANSMEM 302 322 POTENTIAL.
 FT TRANSMEM 583 603 POTENTIAL.
 SQ SEQUENCE 783 AA; 87957 MW; 4DD04F3865C448D2 CRC64;

Query Match 7.1%; Score 90.5; DB 3; Length 783;
 Best Local Similarity 23.3%; Pred. No. 5.3;
 Matches 56; Conservative 34; Mismatches 87; Indels 63; Gaps 12;

QY 10 VLVISASATHEAEQNDVSPPKSRV-----AAQNSAEVVRCLNSALQVGCAGF----- 57
 DB 535 IILMSRPVLLHMKAKNSPRVDRINEDCILAARHLISLVHLQNHSLQSCSYFFDNYNT 594
 QY 58 -----ACLENSTCDTGMVDYCKSPLYSAARFDTQKAFVKESLKCI----- 99
 DB 595 FSSALVLLHCV-TPCEED---DIAMQVAYSALDYMAEGNAKNCARVIRLFDPAHLKG 650
 QY 100 -----ANGVTSKV-FLAIRRCSTFORMIAFVQ-----EECYSKLVNVCSTAKRNPEAITVW 149
 DB 651 ARSDCNGNTSQSGFWA-----WQWIAEVSADPEKLMSPYNSIGGRNSNSLTENA 704
 QY 150 QLPNHFNSRYNR-----LVRSLLCEDTSTIRDSLMKLGKGNMA---SLFPILOTD 200
 DB 705 NIGADVS--FFPTDDTSFLDHSKLDDBLEKFASTLDPI--KTTDPDLANDSSLNWNATD 760

RESULT 8

OC Arabidopsis thaliana (Mouse-ear cress).
 RN NCBI_TaxID=3702;
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RA Vysotskaia V.S., Schwartz J.R., Toriumi M., Yu G., Kwan A., Oji O.,
 RA Liu S., Li J., Araujo R., Au M., Brendel V., Buehler E., Conway A.B.,
 RA Conway A.R., Dewar K., Feng J., Kim C., Kurtz D., Li X., Palm C.J.,
 RA Shinn P., Sun H., Davis R.W., Ecker J.R., Federspiel N.A.,
 RA Theologis A.;
 RT "Arabidopsis thaliana chromosome 1 BAC F1707 sequence.";

RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 RN NCBI_TaxID=4896;
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RA Theologis A.;
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC003671; AAC1813.1; -.
 DR InterPro; IPR000569; HECT_domain.
 DR Pfam; PF00632; HECT; 1.
 DR SMART; SM00119; HECTC; 1.
 DR PROSITE; PS0237; HECT; 1.
 SQ SEQUENCE 1126 AA; 126148 MW; 0DA1A3ACFA8F64E CRC64;

Query Match 7.1%; Score 89.5; DB 10; Length 1126;
 Best Local Similarity 22.1%; Pred. No. 10;
 Matches 46; Conservative 39; Mismatches 76; Indels 47; Gaps 8;

QY 14 SASATHEAEQNDVSPPKSRVAAQNSAEVVRCLNSALQVGCAGFACLENSTCD----- 66
 DB 412 SSETOKDAESELSESVARRK-----NCAEL---YNIPLQLP-----QSDCLNCLMLGY 455
 QY 67 ---TDGMVDICKSPLYSAARFDTQKAFVKESLKCIANGVTSKVFLAIRRCSTFORMIAE 123
 DB 456 EGLSDKIYSLAGEVLKLAADVTVTRKFFTKELSELASGLSSSTVRVLATLSTTKM--- 512
 QY 124 VQECYSKLVNVCSTAKRNPEAITVQVLPNHFNSRYNRVLRSLLCEDTSTIR----- 179
 DB 513 -----SQNTCSMA---GASILRVQLVLSLSTSTIDSDNVGTDKETDQEQINQGLKV 562
 QY 180 --DSLMEKIGPNMASLFIHLQTDHCAQT 205
 DB 563 ALEPLWQELGQCIS--MTELQLDHTAAT 588

RESULT 9

QY 9M7K6 PRELIMINARY; PRT; 3658 AA.
 AC Q9M7K6;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Ubiquitin-protein ligase 2.
 GN UPL2.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 RN NCBI_TaxID=3702;
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RX MEDLINE=20040063; PubMed=10571878;
 RA Bates P.W., Vierstra R.D.;
 RT "UPL1 and 2, two 40S kDa ubiquitin-protein ligases from Arabidopsis
 RL thaliana related to the HECT-domain protein family.";
 RL Plant J. 20:183-195(1999).
 DR EMBL; AF127565; AAF36455.1; -.
 DR InterPro; IPR000569; HECT_domain.
 DR InterPro; IPR002950; Josephin.
 DR InterPro; IPR000449; UBA_domain.
 DR InterPro; IPR003903; UIM.
 DR Pfam; PF00632; HECT; 1.
 DR Pfam; PF00627; UBA; 1.
 DR Pfam; PF02809; UIM; 1.
 DR SMART; SM00119; HECTC; 1.
 DR SMART; SM00165; UBA; 1.
 DR PROSITE; PS0237; HECT; 1.
 KW Ligase.
 SQ SEQUENCE 3658 AA; 403582 MW; 1FB4F8EB8C1F73D1 CRC64;

Query Match 7.1%; Score 89.5; DB 10; Length 3658;
 Best Local Similarity 22.1%; Pred. No. 45;
 Matches 46; Conservative 39; Mismatches 76; Indels 47; Gaps 8;

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QY 14 SASATHEAFQNDVSPKRSVAAQNSAEVVRCLNSALQVCGCAFACLENSTCD----- 66
Db 2977 SSETQDAESELVARRK-----NCAEL-----YNIFLOLP-----QSDLCNLCMLGY 3020

QY 67 ---TGMYDICKSELYSAAKPTQCKAFVKESLKCANGVTSKVFLAIRRCSTFORMIAE 123
Db 3021 ELSKIKYSLAGEVLUKLAANDVTRKFTFKELSELASGLSSSTVRVLATLSTTQRM--- 3077

QY 124 VOECYSKLVNCSIAKRNPFAITEVQVLPNHFNSRYNRLVRSLLCEDEDTVSTIR----- 179
Db 3078 -----SQNTCSMA---GASILRVQLVLSLTSITDSDSVGTGDKETQEQEONIMQGLKV 3127

QY 180 ---DSLMEKIGPNMASLFILOTHCAQT 205
Db 3128 ALEPLWQLGQCIS--MTELQLDHTAAT 3153

RESULT 10
O65029 PRELIMINARY; PRT; 305 AA.
AC O65029;
DT 01-AUG-1998 (Tremblrel. 07, Created)
DT 01-AUG-1998 (Tremblrel. 07, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Peroxidase FLXPER4 (EC 1.11.1.7) (fragment).
GN PER4.
OS Linum usitatissimum (Flax) (Linseed).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Malpighiales; Linaceae; Linum.
OX NCBI_TaxID=4006;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. STORMONT CIRBUS; TISSUE=LEAF;
RA Omann F., Tyson H.;
RT "cDNA sequence of a basic peroxidase (FLXPER4) in flax.";
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF049881; AAC05277.1; --
DR HSSP; P22195; 15CH.
DR InterPro; IPR002016; Peroxidase.
DR Pfam; PF00141; peroxidase; 1.
DR PRINTS; PRO0458; PEROXIDASE.
DR PROSITE; PS00435; PEROXIDASE_1; UNKNOWN_1.
DR PROSITE; PS00436; PEROXIDASE_2; 1.
KW Oxidoreductase; Peroxidase.
FT NON_TER
FT 1
SQ SEQUENCE 305 AA; 32431 MW; F798B1FADP697253 CRC64;

Query Match 7.0%; Score 89; DB 10; Length 305;
Best Local Similarity 21.9%; Pred. No. 2.3;
Matches 57; Conservative 39; Mismatches 92; Indels 72; Gaps 15;

QY 11 LVISATHEAFQNDVSPKRSVAAQNSAEVVRCLNSALQVCGCAFACLENSTCD 68
Db 65 LLLDDTATFTGSKN--AGNQNSV---RGFDIIDITKTRVEAACNATVSCADILAAARD 119

QY 69 GMYDI-----CKSFYSAAKFDTQGFVKESLKCANGVTSKVFLA----- 110
Db 120 GVVLGGTWTVPGLRRDARTASQAANAQIPAG---SSLGTINLFTNKGILTDVIT 176

QY 111 -----IRRCSTFORMIAEVEQECYSKLVN-----CSIAKRN-PEA-----ITEVQLP 152
Db 177 LSGAHTIGQACTTFRQRI-----YNDTNIDPAFTTRRNCQFQAGANLAPLDGTP 229

QY 153 NHFSRYNRLV--RSLLCEDEDTVST--IRDSLMKIGPNMASLFILOTHCAQ----- 204
Db 230 TQFDNRYQDLVARGLLHSDQELFNNGTQDALVRTYSNNAAT-----FATDFAAAMVRMG 285

QY 205 -----THPRADFNRRRTN 217
Db 286 NISPLTGNGEIRFNCRPN 305

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RESULT 11
Q9LUI2 PRELIMINARY; PRT; 1728 AA.
AC Q9LUI2;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
DE Centromere protein.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RX MEDLINE=20277480; PubMed=10819329;
RA Nakamura Y.;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence
RT features of the regions of 4,504,864 bp covered by sixty P1 and TAC
RT clones.";
RL DNA Res. 7:131-135(2000).
DR EMBL; AB022223; BAB01254.1; --
SQ SEQUENCE 1728 AA; 198850 MW; 0F393BC8C939B6D0 CRC64;

Query Match 7.0%; Score 89; DB 10; Length 1728;
Best Local Similarity 21.3%; Pred. No. 20;
Matches 48; Conservative 37; Mismatches 82; Indels 58; Gaps 7;

QY 39 SAEVVRCLNSALQVCGCAFACLENSTCDTDCMYDICKSFYSAAKFDTQGFVK----- 93
Db 459 SQEQKVITSELSQSRIGMLRDLNLEKLEGGDISVKEENQNLSELNDSMIFLETQKE 518

QY 94 -ESLKIANGVTSKVFLAIRRCSTFORMIAEVEQECYS-----KLN 133
Db 519 ISSLKEIKLEEVARHINQSSAFQEIIRLKDIDSLNKRYQAIMQVNLGLDPKSL 578

QY 134 VCSIAKRNPEAITEVQVLPNHFNSRYNRLVRSLLCEDEDTVSTIRDSLMKIGPNMASL 193
Db 579 ACSVRKLQDEN-SKLTCLNHQSD-----KQALTEK-----LREL 613

QY 194 PHILOTDC-----AQTHPRADFNRRRTNEPQKLKVLRLRGEE 233
Db 614 DNILRNKVCLEKLLLESNTKLDGSRKTKD---LQERCESURGEK 655

RESULT 12
Q9LFC2 PRELIMINARY; PRT; 473 AA.
AC Q9LFC2;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
DE Hypothetical 53.5 kDa protein.
GN F7J8_120.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Bevan M., Zimmermann W., Gruenisen A., Wambutt R., Kalicki J.,
RA Wohldmann P., Smith A., Bancroft I., Mewes H.W., Rudd S., Lemcke K.,
RA Mayer K.F.X.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN [2]

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QY 160 YNRLVRSLLCEDDTVSTIRDSLMKIGDNMA-----SLFHIL-----QTDHCAQTHP 207
 Db 117 YRILELI---DSKALKIRD--LQHGHTAGRLMTNEFFAFLMETTVKDVSAICIRSNP 171
 QY 208 RADFNRRRTNEPQKLKVLNLRGE 232
 Db 172 GIDLTR-----LVFVLPKGE 187

RESULT 15

Q9LFC4
 ID Q9LFC4 PRELIMINARY; PRT; 510 AA.
 AC Q9LFC4;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Hypothetical 56.9 kDa protein.
 GN F7J8.100.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bevan M., Zimmermann W., Gruenisen A., Wambutt R., Kalicki J.,
 RA Wohldmann P., Smith A., Bancroft I., Mewes H.W., Rudd S., Lemcke K.,
 RA Mayer K.F.X.;
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL137189; CAB69840.1; -;
 DR InterPro; IPR000923; BlueCu 1.
 DR PROSITE; PS00196; COPPER_BLUE; UNKNOWN_1.
 KW Hypothetical protein.
 SQ SEQUENCE 510 AA; 56940 MW; 9D1D0684F79CFA80 CRC64;

Query Match 6.8%; Score 86; DB 10; Length 510;
 Best Local Similarity 23.5%; Pred. No. 8.3;
 Matches 38; Conservative 22; Mismatches 70; Indels 32; Gaps 5;
 QY 38 NSAEVVRCLNSALQVCGG-----AFACLENSTCTDGMVDICKSFLYSAAKFD----- 85
 Db 108 DDSEATKCFMCPMFRVRSQCCKGSGNFKTSRCS-----CGNFMDEVIQFQEGGCGNG 160
 QY 86 TQKAFVK-----ESLKCIANGVTSKV-----FLAIRRCSTFORMIAEVOEECYSKL 132
 Db 161 SQAEVFRGAHTSFIITDDLKQVNSVSGSTLNLVKDLAYADCCKLVEMILEVNLQEVATL 220
 QY 133 NVCSIAKRNPEAITEVQVLPNHFNSRYNRLVRSLLCEDDT 174
 Db 221 LVCLFTSDTPLTDTFLKKSSHGMRHKRPSPSLSEDEET 262

Search completed: June 12, 2003, 19:56:55
 Job time : 62 secs

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Db 1 GAAACTTCTCAGAGATGCTCCAAAACCTCAGCAGTCTTCTGTGCTGTGATCAGTGT 60
QY 219 TCTGCAACCATGAGCGGAGCAGATGACTCTGTGAGCCCAAGGAAATCCCGAGTGGCG 278
Db 61 TCTGCAACCATGAGCGGAGCAGATGACTCTGTGAGCCCAAGGAAATCCCGAGTGGCG 120
QY 279 GCTCAAAACCTCAGCTGAAGTGGTTCGTGCTCAACAGTGTCTCTACAGTGTGGTGGCG 338
Db 121 GCCAAAACCTCAGCTGAAGTGGTTCGTGCTCAACAGTGTCTCTACAGTGTGGTGGCG 180
QY 339 GCTTTTGCATGCTGGAAGTCCACCTGTGACACAGATGGGATGTACATCTGTAA 398
Db 181 GCTTTTGCATGCTGGAAGTCCACCTGTGACACAGATGGGATGTACATCTGTAA 240
QY 399 TCTCTTCTGTACAGCGCTGCTAAATTTGACACTCAGGAAAGCAATCTGTCAAGAGAGC 458
Db 241 TCTCTTCTGTACAGCGCTGCTAAATTTGACACTCAGGAAAGCAATCTGTCAAGAGAGC 300
QY 459 TTAATAATGCATCGCCAAACGGGTCACCTCCAAGGTCTTCTCGCCATTCGGAGGTCTCC 518
Db 301 TTAATAATGCATCGCCAAACGGGTCACCTCCAAGGTCTTCTCGCCATTCGGAGGTCTCC 360
QY 519 ACTTTTCAAGATGATGCTGAGGTGCAGGAAGAGTGTACAGCAAGCTGAATGTGTGC 578
Db 361 ACTTTTCAAGATGATGCTGAGGTGCAGGAAGAGTGTACAGCAAGCTGAATGTGTGC 420
QY 579 AGCATCGCAAGCGGAACCTGGAAGCCTCAGTGTGCTGAGGTGCTGAGGTGCTGAGGTGCT 638
Db 421 AGCATCGCAAGCGGAACCTGGAAGCCTCAGTGTGCTGAGGTGCTGAGGTGCTGAGGTGCT 480
QY 639 TCAACAGATATATAACAGACTGTGCGAAGCTCTGCGAAGCTCTGCGAAGCTCTGCGAAGCTCT 698
Db 481 TCAACAGATATATAACAGACTGTGCGAAGCTCTGCGAAGCTCTGCGAAGCTCTGCGAAGCTCT 540
QY 699 AGCAATCAGACAGACCTGTGAGGAAATTTGGGCTTAAATGCGGAGCTCTTCCAC 758
Db 541 AGCAATCAGACAGACCTGTGAGGAAATTTGGGCTTAAATGCGGAGCTCTTCCAC 600
QY 759 ATCTCTCAGACAGACCTGTGCGGCAACACACACACAGCTGACCTTCAACAGGAGAGC 818
Db 601 ATCTCTCAGACAGACCTGTGCGGCAACACACACACAGCTGACCTTCAACAGGAGAGC 660
QY 819 ACCAATGAGCGCAGAGCTGAAAGTCTCTCCTCAGGAACCTCGAGGTGAGGAGGACTCT 878
Db 661 ACCAATGAGCGCAGAGCTGAAAGTCTCTCCTCAGGAACCTCGAGGTGAGGAGGACTCT 720
QY 879 CCTCTCCATCAACGCGACATCCATGAGAGTGCATACCAAGGAGAGGT 929
Db 721 CCTCTCCATCAACGCGACATCCATGAGAGTGCATACCAAGGAGAGGT 771
```

RESULT 2
US-09-038-597A-1
; Sequence 1, Application US/09038597A
; Patent No. 5877290
; GENERAL INFORMATION:
; APPLICANT: OLSEN, ET AL.
; TITLE OF INVENTION: Corpiuscles of Stannius Protein,
; TITLE OF INVENTION: Stanniocalcin
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1

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; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/038,597A  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/208,005  
; FILING DATE: 8-MARCH-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: FERRARO, GREGORY D.  
; REGISTRATION NUMBER: 36,134  
; REFERENCE/DOCKET NUMBER: 325800-78  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201-994-1700  
; TELEFAX: 201-994-1744  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 771 BASE PAIRS  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: SINGLE  
; TOPOLOGY: LINEAR  
; MOLECULE TYPE: cDNA  
US-09-038-597A-1  
  
Query Match 20.5%; Score 769.4; DB 2; Length 771;  
Best Local Similarity 99.9%; Pred. No. 5.9e-206;  
Matches 770; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 159 GAAACTTCTCAGAGATGCTCCAAAACCTCAGCAGTGTCTTCTGTGCTGTGATCAGTGT 218  
Db 1 GAAACTTCTCAGAGATGCTCCAAAACCTCAGCAGTGTCTTCTGTGCTGTGATCAGTGT 60  
QY 219 TCTGCAACCATGAGCGGAGCAGAAATGACTCTGTGAGCCCAAGGAAATCCCGAGTGGCG 278  
Db 61 TCTGCAACCATGAGCGGAGCAGAAATGACTCTGTGAGCCCAAGGAAATCCCGAGTGGCG 120  
QY 279 GCTCAAAACCTCAGCTGAAGTGGTTCGTGCTCAACAGTGTCTCTACAGTGTGGTGGCG 338  
Db 121 GCCAAAACCTCAGCTGAAGTGGTTCGTGCTCAACAGTGTCTCTACAGTGTGGTGGCG 180  
QY 339 GCTTTTGCATGCTGGAAGTCCACCTGTGACACAGATGGGATGTACATCTGTAA 398  
Db 181 GCTTTTGCATGCTGGAAGTCCACCTGTGACACAGATGGGATGTACATCTGTAA 240  
QY 399 TCTCTTCTGTACAGCGCTGCTAAATTTGACACTCAGGAAAGCAATCTGTCAAGAGAGC 458  
Db 241 TCTCTTCTGTACAGCGCTGCTAAATTTGACACTCAGGAAAGCAATCTGTCAAGAGAGC 300  
QY 459 TTAATAATGCATCGCCAAACGGGTCACCTCCAAGGTCTTCTCGCCATTCGGAGGTCTCC 518  
Db 301 TTAATAATGCATCGCCAAACGGGTCACCTCCAAGGTCTTCTCGCCATTCGGAGGTCTCC 360  
QY 519 ACTTTTCAAGATGATGCTGAGGTGCAGGAAGAGTGTACAGCAAGCTGAATGTGTGC 578  
Db 361 ACTTTTCAAGATGATGCTGAGGTGCAGGAAGAGTGTACAGCAAGCTGAATGTGTGC 420  
QY 579 AGCATCGCAAGCGGAACCTGGAAGCCTCAGTGTGCTGAGGTGCTGAGGTGCTGAGGTGCT 638  
Db 421 AGCATCGCAAGCGGAACCTGGAAGCCTCAGTGTGCTGAGGTGCTGAGGTGCTGAGGTGCT 480  
QY 639 TCAACAGATATATAACAGACTGTGCGAAGCTCTGCGAAGCTCTGCGAAGCTCTGCGAAGCTCT 698  
Db 481 TCAACAGATATATAACAGACTGTGCGAAGCTCTGCGAAGCTCTGCGAAGCTCTGCGAAGCTCT 540  
QY 699 AGCAATCAGACAGACCTGTGAGGAAATTTGGGCTTAAATGCGGAGCTCTTCCAC 758  
Db 541 AGCAATCAGACAGACCTGTGAGGAAATTTGGGCTTAAATGCGGAGCTCTTCCAC 600  
QY 759 ATCTCTCAGACAGACCTGTGCGGCAACACACACACAGCTGACCTTCAACAGGAGAGC 818  
Db 601 ATCTCTCAGACAGACCTGTGCGGCAACACACACACAGCTGACCTTCAACAGGAGAGC 660  
QY 819 ACCAATGAGCGCAGAGCTGAAAGTCTCTCCTCAGGAACCTCGAGGTGAGGAGGACTCT 878  
Db 661 ACCAATGAGCGCAGAGCTGAAAGTCTCTCCTCAGGAACCTCGAGGTGAGGAGGACTCT 771
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Db 661 ACCAATGAGCCGAGAGCTGAAAGTCTCTCCTCAGGAACCTCCGAGGTGAGGAGACTCT 720
QY 879 CCTCCACATCAAAACGACATCCCATGAGAGTGCATTAACAGGAGAGGT 929
Db 721 CCTCCACATCAAAACGACATCCCATGAGAGTGCATTAACAGGAGAGGT 771

RESULT 3
US-08-431-117A-1
; Sequence 1, Application US/08431117A
; Patent No. 5994301
; GENERAL INFORMATION:
; APPLICANT: OLSEN, ET AL.
; TITLE OF INVENTION: Corpuscles of Stannius Protein, Stannioalcin
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/431,117A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/208,005
; FILING DATE: 8 MARCH 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: FERRARO, GREGORY D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-296
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 771 BASE PAIRS
; TYPE: NUCLEIC ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; MOLECULE TYPE: cDNA
; US-08-431-117A-1

Query Match 20.5%; Score 769.4; DB 2; Length 771;
Best Local Similarity 99.9%; Pred. No. 5.9e-206;
Matches 770; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 159 GAAATCTCTCAGAGATGCTCCAAACTCAGCAGTCTTCTGGTGTGTGATCAGTGTCT 218
Db 1 GAAATCTCTCAGAGATGCTCCAAACTCAGCAGTCTTCTGGTGTGTGATCAGTGTCT 60
QY 219 TCTGCAACCATGAGCGGAGCAGATGACTCTGTGAGCCCGAGGAAATCCCGAGTGGCG 278
Db 61 TCTGCAACCATGAGCGGAGCAGATGACTCTGTGAGCCCGAGGAAATCCCGAGTGGCG 120
QY 279 GCTCAAAACTCAGTCAAGTGGTTCCTTCAACAGTCTCTACAGTTCGCTGCGGCG 338
Db 121 GCCCAAACTCAGTCAAGTGGTTCCTTCAACAGTCTCTACAGTTCGCTGCGGCG 180
QY 339 GCTTTTGCATGCTGGAAACTCCACTGTGACACAGATGGGATGATGACATCTGTAAA 398
Db 181 GCTTTTGCATGCTGGAAACTCCACTGTGACACAGATGGGATGATGACATCTGTAAA 240
QY 399 TCGTCTTGTACAGCGCTCTAAATTGACATCTAGGGAAGAGCATTCCTCAAGAGAGC 458

Db 241 TCCTTCTTGTACAGCGCTGCTAAATTTTGACACTCAGGGGAAAAAGCATTCCTCAAGAGAGC 300
QY 459 TTTAAATGATCATCGCAACGGGGTCACTCCAAAGGTCTTCTCGCCATTTCGGAGGTCTCTCC 518
Db 301 TTTAAATGATCATCGCAACGGGGTCACTCCAAAGGTCTTCTCGCCATTTCGGAGGTCTCTCC 360
QY 519 ACTTTCCAAAGGATGATTGCTGAGGTGTCAGGAAGAGTGTACAGCAAGCTGAATGTGTGC 578
Db 361 ACTTTCCAAAGGATGATTGCTGAGGTGTCAGGAAGAGTGTACAGCAAGCTGAATGTGTGC 420
QY 579 AGCATCGCCCAAGCGGAAACCTTGAAGCCATCATCTGAGGTCTCCAGTGCCTCCCAATCACTTC 638
Db 421 AGCATCGCCCAAGCGGAAACCTTGAAGCCATCATCTGAGGTCTCCAGTGCCTCCCAATCACTTC 480
QY 639 TCCAAACAGATACTATAACAGACTTGTCCGAAGCCCTGCTGGAATGTGATGAAGACACAGTC 698
Db 481 TCCAAACAGATACTATAACAGACTTGTCCGAAGCCCTGCTGGAATGTGATGAAGACACAGTC 540
QY 699 AGCAATCAGAGACAGCCTGTATGGAGAAATTTGGGCTTAAATGAGCCAGCTCTTTCCAC 758
Db 541 AGCAATCAGAGACAGCCTGTATGGAGAAATTTGGGCTTAAATGAGCCAGCTCTTTCCAC 600
QY 759 ATCTTGCAGACAGACACTGTGCCCCAAACACACACACACAGCTTCAACAGGAGAGC 818
Db 601 ATCTTGCAGACAGACACTGTGCCCCAAACACACACACACAGCTTCAACAGGAGAGC 660
QY 819 ACCAATGAGCCGACAGAGCTGAAAGTCTCTCCTCAGGAACCTCCGAGGTGAGGAGACTCT 878
Db 661 ACCAATGAGCCGACAGAGCTGAAAGTCTCTCCTCAGGAACCTCCGAGGTGAGGAGACTCT 720
QY 879 CCTTCCCATCAAAACGACATCCCATGAGAGTGCATTAACAGGAGAGGT 929
Db 721 CCTTCCCATCAAAACGACATCCCATGAGAGTGCATTAACAGGAGAGGT 771

RESULT 4
US-08-831-132-1
; Sequence 1, Application US/08831132
; Patent No. 6008322
; GENERAL INFORMATION:
; APPLICANT: Kuestner, Rolf E.
; APPLICANT: Konlin, Darrell C.
; APPLICANT: Lok, Si
; APPLICANT: Buddle, Michele
; APPLICANT: Downey, William
; TITLE OF INVENTION: STANNIOCALCIN-2
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/831,132
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A.
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 96-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6672
; TELEFAX: 206-442-6678
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 906 base pairs

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 1.72
NAME/KEY: mat_peptide
LOCATION: 73..906
FEATURE:
NAME/KEY: CDS
LOCATION: 1..906
US-08-831-132-1

Query Match 3.3%; Score 122.8; DB 3; Length 906;
Best Local Similarity 52.8%; Pred. No. 1.8e-24;
Matches 265; Conservative 0; Mismatches 237; Indels 0; Gaps 0;

QY 263 GAAATCCCGAGTGGCGGCTCAAAACTCAGCTGAAGTGGTTGCTGCTCAACAGTGTCTCT 322
DB 123 GAAAGCGCGCTGTCTCTGAGATACAGGGAGATCCAGCACTGTTTGGTCAACGCTGG 182
QY 323 ACAGTGGCTGGCGGCTTTTCATGCTCTGGAATACTCCACTGTGACACAGATGGAT 382
DB 183 CGATGTGGGTGGCGGTGTTGAATGTTTCGAGAACAACTCTGTGAGATTCCGGGCTT 242
QY 383 GTATGACATCTGTAATCTCTTGTACAGCGCTGCTAAATTTGACACTCAGGGAAGC 442
DB 243 ACATGGATTGTCATGACTTTTCTGCACAACTGGAATAATTTGATGCCCGGCAAGTC 302
QY 443 ATTCTGTCAGAGAGCTTAAATGCTCGCAACGGGCTCACCTCCAAAGTCTTCTCTCG 502
DB 303 ATTCTGTCAGAGAGCTTAAATGCTCGCAACGGGCTCACCTCCAAAGTCTTCTCTCG 362
QY 503 CATTCGAGGTGCTCACTTTTCAAGAGATGATGTTGAGGTGCGAGAAAGATGCTACAG 562
DB 363 AAGCGGAAGTGGCGGCTATCAGGGAATGTTGTCAGTTCAGCGGAATGCTACCT 422
QY 563 CRAAGTGAATGTTGAGCATGCGCAACGGGCTGAGGAGCTTGAAGCTCAGTGTGCTCA 622
DB 423 CAAGCAGAGCTTGGCGGCTGCCAGGAGAACACCCGGGTGATAGTGAGATGATCA 482
QY 623 GCTGCCCAATCACTTCTCCAAAGATGATGTTGAGGTGCGAGAAAGATGCTACAG 682
DB 483 TTTCAAGGACTTCTGTCGACGAACTTACGTTGAGCTTGTGCTGACCTG 542
QY 683 TGATGAAGACAGTCAAGCAATCAGACAGCTGATGGAGAAATTTGGGCTTAACAT 742
DB 543 TGGGAGAGGTGAAGAGGCTATCCCAAGCTGACAGCTGAGTGTGAGCAGAACTG 602
QY 743 GGCCAGCTTCTCCATCTG 764
DB 603 GGAAGCCTGTGCTCATCTG 624

RESULT 5
US-09-416-150-1
Sequence 1, Application US/09416150
Patent No. 671822
GENERAL INFORMATION:
APPLICANT: Kuestner, Rolf E.
Lok, Si
Buddle, Michele
Downey, William
TITLE OF INVENTION: STANNIOALCIN-2
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
STATE: WA

COUNTRY: USA
ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/416,150
FILING DATE: 11-Oct-1999
CLASSIFICATION: <Unknown>
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/831,132
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Sawislak, Deborah A.
REGISTRATION NUMBER: 37,438
REFERENCE/DOCKET NUMBER: 96-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6672
TELEFAX: 206-442-6678
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 906 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 1.72
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 73..906
FEATURE:
NAME/KEY: CDS
LOCATION: 1..906
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-416-150-1

Query Match 3.3%; Score 122.8; DB 4; Length 906;
Best Local Similarity 52.8%; Pred. No. 1.8e-24;
Matches 265; Conservative 0; Mismatches 237; Indels 0; Gaps 0;

QY 263 GAAATCCCGAGTGGCGGCTCAAAACTCAGCTGAAGTGGTTGCTGCTCAACAGTGTCTCT 322
DB 123 GAAAGCGCGCTGTCTCTGAGATACAGGGAGATCCAGCACTGTTTGGTCAACGCTGG 182
QY 323 ACAGTGGCTGGCGGCTTTTTCATGCTCTGGAATACTCCACTGTGACACAGATGGAT 382
DB 183 CGATGTGGGTGGCGGTGTTGAATGTTTCGAGAACAACTCTGTGAGATTCCGGGCTT 242
QY 383 GTATGACATCTGTAATCTCTTGTACAGCGCTGCTAAATTTGACACTCAGGGAAGC 442
DB 243 ACATGGATTGTCATGACTTTTCTGCACAACTGGAATAATTTGATGCCCGGCAAGTC 302
QY 443 ATTCTGTCAGAGAGCTTAAATGCTCGCAACGGGCTCACCTCCAAAGTCTTCTCTCG 502
DB 303 ATTCTGTCAGAGAGCTTAAATGCTCGCAACGGGCTCACCTCCAAAGTCTTCTCTCG 362
QY 503 CATTCGAGGTGCTCACTTTTCAAGAGATGATGTTGAGGTGCGAGAAAGATGCTACAG 562
DB 363 AAGCGGAAGTGGCGGCTATCAGGGAATGTTGTCAGTTCAGCGGAATGCTACCT 422
QY 563 CRAAGTGAATGTTGAGCATGCGCAACGGGCTGAGGAGCTTGAAGCTCAGTGTGCTCA 622
DB 423 CAAGCAGAGCTTGGCGGCTGCCAGGAGAACACCCGGGTGATAGTGAGATGATCA 482
QY 623 GCTGCCCAATCACTTCTCCAAAGATGATGTTGAGGTGCGAGAAAGATGCTACAG 682
DB 483 TTTCAAGGACTTCTGTCGACGAACTTACGTTGAGCTTGTGCTGACCTG 542
QY 683 TGATGAAGACAGTCAAGCAATCAGACAGCTGATGGAGAAATTTGGGCTTAACAT 742
DB 543 TGGGAGAGGTGAAGAGGCTATCCCAAGCTGACAGCTGAGTGTGAGCAGAACTG 602
QY 743 GGCCAGCTTCTCCATCTG 764
DB 603 GGAAGCCTGTGCTCATCTG 624

Db 543 TGGGAGGAGGTGAAGAGGCCATCACCCAGCGTGCAGGTTCACTGTGAGCAGAACTG 602
QY 743 GGCCAGCCTCTTCCACATCCTG 764
Db 603 GGAAGCCTGTGCTCCATCTTG 624

RESULT 6
US-08-460-529B-1
; Sequence 1, Application US/08460529B
; Patent No. 5994103
; GENERAL INFORMATION:
; APPLICANT: OLSEN, ET AL.
; TITLE OF INVENTION: Human Stanniocalcin-alpha
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,529B
; FILING DATE: June 2, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/13206
; FILING DATE: 10 NOV 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-334 (PF143)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 892 BASE PAIRS
; TYPE: NUCLEIC ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; MOLECULE TYPE: CDNA
US-08-460-529B-1

Query Match 3.2%; Score 121.2; DB 2; Length 892;
Best Local Similarity 52.6%; Pred. No. 5.1e-24;
Matches 264; Conservative 0; Mismatches 238; Indels 0; Gaps 0;

QY 263 GAAATCCGAGTGGGGCTCAAACTCAGCTGAAGTGGTTCGTCCTCAACAGTGCCT 322
Db 204 GAAAGCCGCTGTCCTCGACAGATACAGCGAGATCCAGCACTGTTGGTCAACGCTGG 263
QY 323 ACAGTCGGCTCGGGGCTTTGATGCTGCTGAAACTCCACTGTGACACAGATGGAT 382
Db 264 CGATGCGGGTGTGGGCTTTGATGCTGCTGAAACTCCACTGTGAGATTTCGGGGCTT 323
QY 383 GTATGATCTCTAAATCTCTTGTACAGCGCTGCTAAATTTGACATCCAGGGAAGC 442
Db 324 ACATGGGATTTGCATGACTTTTCTGCACAACTGCTGAAATTTGATGCCAGGGCAAGTC 383
QY 443 ATTGCTCAAGAGAGCTTAAATATGATCGCCAACTGGGTTCACCTCCAAAGGTTCTTCTCGC 502
Db 384 ATTATCAAGAGCGCTTGAATGTAAAGCCCACTCTGCGGCACAGGTTTCGGTGTGAT 443
QY 503 CATTGCGAGGTCTCTCACTTTTCCAAAGGATGATGCTGAGGTGCAGGAAGAGTGTCTACAG 562

Db 444 AAGCCGGAAGTCCCGGCCATCAGGGAATGTTGTCCAGTTGGAGCGGAATGCTACT 503
QY 563 CAAGCTGAATGTGTGAGCATCGCCAAAGCGGAACCTGAAGCCATCACTGAGGTGCTCCA 622
Db 504 CAAGCAGCACCTGTGCGGGTCCCGAGGAGAACCCGGGTGATAGTGGAGATGATCCA 563
QY 623 GCTGCCCAATCACTTCTCCACAGATATATATAAGACTTTGTCGGAAGCCTCTCTGGAATG 682
Db 564 TTTCAAGGACTTGTGCTGCACGAACCTCTACGTGGACCTCGTGAACCTTGTCTGACCTG 623
QY 683 TGATGAAGACACAGTCAGCACAATCAGACAGACCTGATGGAGAAAATTTGGCCCTAACAT 742
Db 624 TGGGAGGAGGTGAAGGAGGCCATCACCCACAGCGTGCAGGTTTCACTGTGAGCAGAACTG 683
QY 743 GGCCAGCCTCTTCCACATCCTG 764
Db 684 GGAAGCCTGTGCTCCATCTTG 705

RESULT 7
US-08-831-132-13
; Sequence 13, Application US/08831132
; Patent No. 6008322
; GENERAL INFORMATION:
; APPLICANT: Kuestner, Rolf E.
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Lok, Si
; APPLICANT: Buddle, Michele
; APPLICANT: Downey, William
; TITLE OF INVENTION: STANNIOCALCIN-2
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/831,132
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A.
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 96-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6672
; TELEFAX: 206-442-6678
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 888 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 1..72
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 73..888
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..888
US-08-831-132-13


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/ FILING DATE: 23-MAR-1998
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Cawley, Jr., Thomas A.
/ REGISTRATION NUMBER: 40,944
/ REFERENCE/DOCKET NUMBER: 19036/36276
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (312) 474-6300
/ TELEFAX: (312) 474-0448
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1988 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ ORIGINAL SOURCE:
/ ORGANISM: Klebsiella pneumoniae
/ STRAIN: Clinical isolate KP-98-22
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: 1930-
/ OTHER INFORMATION: /note= "N= adenine or cytosine or
/ OTHER INFORMATION: guanine or thymine"
US-09-402-002-3

Query Match 1.2%; Score 43.4; DB 4; Length 1988;
Best Local Similarity 50.7%; Pred. No. 0.057;
Matches 104; Conservative 0; Mismatches 101; Indels 0; Gaps 0;

QY 3479 TTATATTGCAATATGATTTATTAATTAATGATATTTAGTTTGGCTGAGTACTGG 3538
Db 206 TCATTATTTCCTTTGTTTCCTGTTTATTATTAATGCTAATTAATAATATATTTGTT 147
QY 3539 AATAACAGTGACATATCTGATATGCTATGCTATTTATTTTAAATACATTTTAAAGC 3598
Db 146 CAATAATATTACACATCTGACTATATTAATTTGTTGTTATTTATTTATTTATGTAAGC 87
QY 3599 TCCATGTCATATAAGGTTATGAAACATATCATGTTAATGACAGATGCAAGTTATTTTA 3658
Db 86 CAAATAAATAATAAGGATACGAAACAAATAACATACAAATGAGAAAGTTATGAAG 27
QY 3659 TTGCTTATTATTATTAATTAAGAT 3683
Db 26 AAGAAAAATCTTTTATTTCTTAAGCT 2

RESULT 12
US-09-014-969-14/c
; Sequence 14, Application US/09014969
; Patent No. 5965397
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: Lavallie, Edward R.
; APPLICANT: Racie, Lisa A.
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Spaulding, Vikki
; APPLICANT: Agostino, Michael J.
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PC-DOS/MS-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09014969
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07935313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:

/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/014,969
/ FILING DATE:
/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Sprunger, Suzanne A.
/ REGISTRATION NUMBER: 41,323
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (617) 498-8284
/ TELEFAX: (617) 876-5851
/ INFORMATION FOR SEQ ID NO: 14:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 2447 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
US-09-014-969-14

Query Match 1.1%; Score 43.2; DB 2; Length 2447;
Best Local Similarity 53.2%; Pred. No. 0.074;
Matches 84; Conservative 1; Mismatches 73; Indels 0; Gaps 0;

QY 3137 TTCTCTCTTTTCAGTTTCAGTAGATTTCCTTTTCTTTCTTTCTTTTCTTTTCTTTT 3196
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Db 2255 TTTTCTTTTCTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 2196
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Db 2195 GATCCAGATATGTGAACCATATATACATATCTATACAG 2158

RESULT 13
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PC-DOS/MS-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
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QY	3484	TTTGCATTATGTATTTATATAATTTAAATGATATTTAGGTTTTTGGCTGAGTACTTGGAAATAA	3543							
Db	456	TTTGTAAATTTTATTATTATTTTTCATATCTCTGCACCTGCTGTAGCATTTGAATTCT	397							
QY	3544	ACAGTGAGCATATCTGGTATATGTCATTTATTTGTTAAATACATTTTAAAGCTCCAT	3603							
Db	396	AGGATCAAAATGTTCAATGAAATGTTTTTAATTTTGTACAGTATCATTTTGTGGATCAAT	337							
QY	3604	GTGCATATAAAGGTTTATGAAACATATCATGTTAATGACAGATGCAAGTTATTTTATTTCG	3663							
Db	336	TGTAATGAAATTTACTTTGTAACCTTGTGTCATTTACCAAGCTGTGAGAGAACTTCAGA	277							
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Db	276	TGCTATTCCTAATTCAGAGGGCAGATGCTTTTA	243							

Search completed: June 9, 2003, 13:11:14
 Job time : 206 secs

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RESULT 2
 US-10-198-846-13651
 ; Sequence 13651, Application US/10198846
 ; Publication No. US2003009974A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lillie, James
 ; APPLICANT: Xu, Yongyao
 ; APPLICANT: Wang, Youzhen
 ; APPLICANT: Steinmann, Kathleen
 ; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
 ; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
 ; FILE REFERENCE: MRI-049
 ; CURRENT APPLICATION NUMBER: US/10/198,846
 ; CURRENT FILING DATE: 2002-07-18
 ; PRIOR APPLICATION NUMBER: 60/306,220
 ; PRIOR FILING DATE: 2001-07-18
 ; NUMBER OF SEQ ID NOS: 14084
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 13651
 ; LENGTH: 3897
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: 3878, 3879, 3880, 3881, 3882, 3883, 3884, 3885, 3886, 3887,
 ; LOCATION: 3888, 3889, 3890, 3891, 3892, 3893, 3894, 3895, 3896, 3897
 ; OTHER INFORMATION: n = A,T,C or G
 US-10-198-846-13651

Query Match 97.0%; Score 3650.6; DB 9; Length 3897;
 Best Local Similarity 97.8%; Pred. No. 0;
 Matches 3680; Conservative 0; Mismatches 80; Indels 4; Gaps 2;

QY 1 GGTGCGAGCAGCATCACAGTTAACCAACAAAAAATCTCTCAATCAATCTCTAC 60
 Db 112 GGTGCGAGCAGCATCACAGTTAACCAACAAAAAATCTCTCAATCAATCTCTAC 171
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 Db 172 CTAACTTTCAGTGTATCCAGATCCACATCTTCACTCAAGCCAGGAGGGAAGGAA 231
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 QY 2041 AAAGAGCA-CCCTATGGGCTTGACACCTTACAGTGTGATAAGGCTACTATACATTAGS 2099
 Db 2152 AAAGAGCACTCCCTATGGGCTTGACACCTTACAGTGTGATAAGGCTACTATACATTAGS 2211
 QY 2100 AAGTGGCAGTTCTTTTACTGCTCCCTTTTCACTCGGTGCTGTTACTCTGCAAAATGATGAT 2159
 Db 2212 AAGTGGCAGTTCTTTTACTGCTCCCTTTTCACTCGGTGCTGTTACTCTGCAAAATGATGAT 2271
 QY 2160 GGGGTGGAGACTTTCCATTTAAATCAATCAGGAATGAGTCAATCAGCCTTTTAGTCTTTA 2219
 Db 2272 GGGGTGGAGACTTTCCATTTAAATCAATCAGGAATGAGTCAATCAGCCTTTTAGTCTTTA 2331
 QY 2220 GTCCGGGAGCTTTGGGCTTGAGAGATATAAATACCCCTGGGCTGTCCAGCCTTTAATAGA 2279
 Db 2332 GTCCGGGAGCTTTGGGCTTGAGAGATATAAATACCCCTGGGCTGTCCAGCCTTTAATAGA 2391
 QY 2280 CTTCTCTTACATTTTCTGCTCTGACAGCTGCTCCCAAGTAGTCTCTGGCAGCTGGAC 2339
 Db 2392 CTTCTCTTACATTTTCTGCTCTGACAGCTGCTCCCAAGTAGTCTCTGGCAGCTGGAC 2451
 QY 2340 CATCTCTGTAGGATCGTAAAAAATAGAAAAAATAGAAAAAATAGAAAAAATAGAAAAA 2399
 Db 2452 CATCTCTGTAGGATCGTAAAAAATAGAAAAAATAGAAAAAATAGAAAAAATAGAAAAA 2511
 QY 2400 NNNNNCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 2459
 Db 2512 AAGAGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 2571
 QY 2460 AAACGACTAACCTATCTATGAACAAACAGTAGTTTCTCAGGGTCACTGTCTTGAACCCAA 2519

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2572 AAAAGCACTAATCTATATGAACAAACAGTAGTTTCTCAGGGTCACTGTCTTTGAACCCAA 2631
2520 CAGTCCCTTTAGAGCGTCACTGCCACCAAGGTCAATGTCAAGAGAGAGAGAGAGAG 2579
2632 CAGTCCCTTTAGAGCGTCACTGCCACCAAGGTCAATGTCAAGAGAGAGAGAGAGAG 2691
2580 GAGGGTAGGACTGACGAGGGGCCACTCCAACTCGCTTAGGTAGAACTATTGGTCTTGA 2639
2692 GAGGGTAGGACTGACGAGGGGCCACTCCAACTCGCTTAGGTAGAACTATTGGTCTTGA 2751
2640 CTCTCACTAGGCTAACTCAAGATTGACCAATCGAGTGATAGGATCCTGGTGGGAGG 2699
2752 CTCTCACTAGGCTAACTCAAGATTGACCAATCGAGTGATAGGATCCTGGTGGGAGG 2811
2700 AGAGAGGGCACATCTCCAGAAAAAAGAAAGCAATACAACTTTACCATAAAGCCTTTAA 2759
2812 AGAGAGGGCACATCTCCAGAAAAAAGAAAGCAATACAACTTTACCATAAAGCCTTTAA 2871
2760 ACCAGTAACGTGCTGCTCAAGGACCAAGAGCAATTTNNNNNNNNNNNNNNNNNNNN 2819
2872 ACCAGTAACGTGCTGCTCAAGGACCAAGAGCAATTTGCAGCAGACCCAGCAGCAG 2931
2820 NNNNNCAACATTGCTGCTTTGTCCCCACACAGCCTCTAAGGCTGCTGACATCAGATTG 2879
2932 CAGCAACAACTGCTGCTGCTTTGTCCCCACACAGCCTCTAAGGCTGCTGACATCAGATTG 2991
2880 TTAAGGGCAATTTTATACTCAGAACTGCTCCCATCCAGGTCCTCCAACTTATGACACT 2939
2992 TTAAGGGCAATTTTATACTCAGAACTGCTCCCATCCAGGTCCTCCAACTTATGACACT 3051
2940 GCCTTAGCCTCTTGGAAATCAGGTAGACCATATTCTAAGTTAGACTCTTCCCTCCCTCC 2999
3052 GCCTTAGCCTCTTGGAAATCAGGTAGACCATATTCTAAGTTAGACTCTTCCCTCCCTCC 3111
3000 CACACTTCCACCCAGCAGAGGCTGACTCTCTGAATCAGAAAGCTATTAAAGTTTG 3059
3112 CACACTTCCACCCAGCAGAGGCTGACTCTCTGAATCAGAAAGCTATTAAAGTTTG 3171
3060 TGTGTTGCTGCATTTTGAACCCCACTAAGCAGGACCCCAATGCGACAAAGTAGTTCA 3119
3172 TGTGTTGCTGCATTTTGAACCCCACTAAGCAGGACCCCAATGCGACAAAGTAGTTCA 3231
3120 TGAGTATCTCAGCAAAATTTCTCTTTCTTCTCAGTTAGTAGATTTCCTTTTCTTNTC 3179
3232 TGAGTATCTCAGCAAAATTTCTCTTTCTTCTCAGTTAGTAGATTTCCTTTTCTTTTC 3291
3180 ---TWTWTWTWTWTWTWTGCTGTGACCTCTTCAACCGTGGTACCCCTCCCTTTTC 3236
3292 TTTTTTTTTTTTTTTTTTTTTTGGCTGTGACCTCTTCAACCGTGGTACCCCTCCCTTTTC 3351
3237 TCCCAACGATGATATCTATATGTATCTACAAATACATATATCTACACATACAGAAAGAA 3296
3352 TCCCAACGATGATATCTATATGTATCTACAAATACATATATCTACACATACAGAAAGAA 3411
3297 GCAGTTCTCACAATGTGCTAGTTTTTGTCTTCTCTTCCCAACCCCTACTCCCTCCAA 3356
3412 GCAGTTCTCACAATGTGCTAGTTTTTGTCTTCTCTTCTTCCCAACCCCTACTCCCTCCAA 3471
3357 TCCCTCTTAACTTCAAGAGCTTGTCTTGTGTTGCTGACAGTAGATTTCGGGGGCTGAC 3416
3472 TCCCTCTTAACTTCAAGAGCTTGTCTTGTGTTGCTGACAGTAGATTTCGGGGGCTGAC 3531
3417 CTAGACAGTTTGCATGATTCTTCTCTGTGATTGTTGCTGACATTAGACATTTTGTGC 3476
3532 CTAGACAGTTTGCATGATTCTTCTCTGTGATTGTTGCTGACATTAGACATTTTGTGC 3591
3477 CATTATATTGCAATGATTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3536
3592 CATTATATTGCAATGATTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3651
3537 GGAATAACAGTGAGCATATCTGGTATATGTCATTTATTTATTTATTAATTAATTTAA 3596

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3652 GGAATAAACAGTAGACATATCTGGTATATGTCATTTATTTATTTGTTAAATTAATTTTAA 3711
3597 GCTCCATGTGCATATAAAGGTTTATGAAACATATCATGTGTAATGACAGATGCAAGTTATTT 3656
3712 GCTCCATGTGCATATAAAGGTTTATGAAACATATCATGTGTAATGACAGATGCAAGTTATTT 3771
3657 TATTTGCTTATTTTATTAATTAAGATGCCATAGCATATATGAAGCCTTTTGGTGAATTC 3716
3772 TATTTGCTTATTTTATTAATTAAGATGCCATAGCATATATGAAGCCTTTTGGTGAATTC 3831
3717 CTCTCAAGTAAAAATAATAATAAAGTGTAGGTTTATTTGTT 3760
3832 CTCTCAAGTAAAAATAATAATAAAGTGTAGGTTTATTTGTT 3875

RESULT 3
US-09-925-300-486
; Sequence 486, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Steve Ruben,
; APPLICANT: Craig Rosen,
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925,300
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 486
; LENGTH: 2572
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (823)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-300-486

Query Match 61.4%; Score 2311.6; DB 10; Length 2572;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 2344; Conservative 4; Mismatches 3; Indels 3; Gaps 3;

QY 1 GGTGCACAGCAGCATCACAGCTAACACACAAAAAATCTCATCAATCCTCAC 60
DB 92 GGTGCACAGCAGCATCACAGCAGCAACAAACAAAAATCTCATCAATCCTCAC 151
QY 61 CTAAGCTTTTCAGTGTATCCAGATCCACATCTTCACTCAAGCCAGGAGGAAAGGAA 120
DB 152 CTAAGCTTTTCAGTGTATCCAGATCCACATCTTCACTCAAGCCAGGAGGAAAGGAA 211
QY 121 AGGGGGCAGGAAAAAAGAAAAAAGCCAACTTACAGCGAAATCTTCTCAGAAATGCTCC 180
DB 212 AGGGGGCAGGAAAAAAGAAAAAAGCCAACTTACAGCGAAATCTTCTCAGAAATGCTCC 271
QY 181 AAAACTCAGCAGTGTCTTCTGCTGCTGATCAGTGTCTTCTGCAACCCATGAGCGGAGC 240
DB 272 AAAACTCAGCAGTGTCTTCTGCTGCTGATCAGTGTCTTCTGCAACCCATGAGCGGAGC 331
QY 241 AGAATGACTCTGTGAGCCCCAGGAAATCCGAGTGGCGGCTCAAAACTCAGCTGAAGTGG 300
DB 332 AGAATGACTCTGTGAGCCCCAGGAAATCCGAGTGGCGGCTCAAAACTCAGCTGAAGTGG 391
QY 301 TTGCTTGCCTCAACAGTGTCTTACAGGTGGCTGCGGGGCTTTTGCATCGCTGGAAGT 360
DB 392 TTGCTTGCCTCAACAGTGTCTTACAGGTGGCTGCGGGGCTTTTGCATCGCTGGAAGT 451
QY 361 CCACCTGTGACACAGATGGGATGTATGACATCTGTAATCTCTTTGTACAGCGCTGCTA 420
DB 452 CCACCTGTGACACAGATGGGATGTATGACATCTGTAATCTCTTTGTACAGCGCTGCTA 511

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QY 421 AATTTGACACTCAGGGAAGCAATTCCTCAAGAGAGCTTTAAATGCAATCGCCAAACGGGG 480
 DB |||||
 QY 512 AATTTGACACTCAGGGAAGCAATTCCTCAAGAGAGCTTTAAATGCAATCGCCAAACGGGG 571
 DB |||||
 QY 481 TCACCTCCAAAGGCTTCCTCGCCCAATTCGGAGGTCCTCAATTTCCAAAAGATGATGCTG 540
 DB |||||
 QY 572 TCACCTCCAAAGGCTTCCTCGCCCAATTCGGAGGTCCTCAATTTCCAAAAGATGATGCTG 631
 DB |||||
 QY 541 AGGTGAGAGAGAGTCTCAGCAAGCTGAATGCTGTCAGCAGTCGCAAGCGGAACCCCTG 600
 DB |||||
 QY 632 AGGTGAGAGAGAGTCTCAGCAAGCTGAATGCTGTCAGCAGTCGCAAGCGGAACCCCTG 691
 DB |||||
 QY 601 AAGCCATCACTAGAGTCTGTCAGCTGCCCAATCACTTCTCCAAACAGATACTATAACAGAC 660
 DB |||||
 QY 692 AAGCCATCACTAGAGTCTGTCAGCTGCCCAATCACTTCTCCAAACAGATACTATAACAGAC 751
 DB |||||
 QY 661 TTGTCGAGAGCTGCTGGAATGATGAAGACACAGTCAAGCAATCAAGACAGCCTGA 720
 DB |||||
 QY 752 TTGTCGAGAGCTGCTGGAATGATGAAGACACAGTCAAGCAATCAAGACAGCCTGA 811
 DB |||||
 QY 721 TGGAGAAATTTGGGCTTAACATGCGCAGCTCTCCACATCTGTCAGACAGACCACTGT 779
 DB |||||
 QY 812 TGGAGAAATTTGGGCTTAACATGCGCAGCTCTCCACATCTGTCAGACAGACCACTGT 871
 DB |||||
 QY 780 GCCCAACACACCCAGAGCTGACTTCAACAGGAGACGCAACCAATGAGCGCGAGAGCTG 839
 DB |||||
 QY 872 GCCCAACACACCCAGAGCTGACTTCAACAGGAGACGCAACCAATGAGCGCGAGAGCTG 931
 DB |||||
 QY 840 AAAGTCTCTCAGGAACCTCCGAGTGAGGAGCTCTCCCTCCCAATCAAGACGACCA 899
 DB |||||
 QY 932 AAAGTCTCTCAGGAACCTCCGAGTGAGGAGCTCTCCCTCCCAATCAAGACGACCA 991
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 QY 900 TCCCATGAGTGATCAACAGGAGAGGTATTCAACACCTCACCACCACTAGTATCAT 959
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 QY 1020 GTTCTCTATTTCTATCCCTTAAAGAAATTTGATGAAATTTGATGAAATTTGATGAAAT 1079
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 QY 1112 GTTCTCTATTTCTATCCCTTAAAGAAATTTGATGAAATTTGATGAAATTTGATGAAAT 1171
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 QY 1172 TCCCAACATTCGCAATGAGAGCTTCCCAACCAACCAATTCATGTCAGTATTCGCTC 1231
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 QY 1140 TCCCAAGGAGAGTACCTCTTTTACCAATTCCTCTGCTGCTGCTGCTGCTGCTGCTGCTG 1199
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 QY 1292 CTGAGACACCCCAACCAACCAATTCATGTAATTCCTCCAGCCTGTAATTTGAAGA 1351
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 DB |||||
 QY 1352 TGTGGATCCCTTTAGAACGTTGCCCGAGTAGGTTAGCTGATAGGAACCTTTATTAA 1411
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 QY 1320 ATGCATGCTCTTAATGCTCATGAAGATTTAAATGGAATTCGTGTTATGAATCTGTGCTG 1379
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 QY 1412 ATGCATGCTCTTAATGCTCATGAAGATTTAAATGGAATTCGTGTTATGAATCTGTGCTG 1471
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 QY 1380 GGCATGGAGATATGAATGTCACATTTGAAATTCCTGATCTCTTAATGAGCTAGTGTCTTA 1439
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 QY 1472 GGCATGGAGATATGAATGTCACATTTGAAATTCCTGATCTCTTAATGAGCTAGTGTCTTA 1531
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 QY 1440 TGTGCTTTGATCCTCCATGCTAAATTTCTTCCGACACATTTACCAATTCCTTGAGCC 1499
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 DB |||||

QY 1500 TGGCTGTCAACACAGACTTTGAGCTGCTCATCTTTTGCATCTTAATGAAAAACAAAGCT 1559
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 QY 1560 AACATCTTTACGTACTGTAACCTGCTCAGAGCTTTTAAAGTATCTTTTAAACAATGCTTAA 1619
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 QY 1652 AACATCTTTACGTACTGTAACCTGCTCAGAGCTTTTAAAGTATCTTTTAAACAATGCTTAA 1711
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 QY 1620 AACACAGAACTCTTAAGGTCTAACTGCTGAATATATAAGCTGAAAACTTAATGCTACTGTA 1679
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 QY 1680 CATAAATTTCCAGAGACTCTGCTTAAACAAAGCAGTATATAATACTTTTATTCATATAG 1739
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 QY 1772 CATAAATTTCCAGAGACTCTGCTTAAACAAAGCAGTATATAATACTTTTATTCATATAG 1831
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 QY 1800 TCCAGATATCCACATAAATGCTCTTGTGGCCTTTTATTAACCTAAAGGGGTAGAGTAG 1859
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 QY 1892 TCCAGATATCCACATAAATGCTCTTGTGGCCTTTTATTAACCTAAAGGGGTAGAGTAG 1951
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 QY 1860 TTTTAAATTTCAACATCAAACTTTAAGATGGCCTGTATGAGACAGGAAAAACCAAGCTT 1919
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 QY 1952 TTTTAAATTTCAACATCAAACTTTAAGATGGCCTGTATGAGACAGGAAAAACCAAGCTT 2011
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 QY 1920 TATCTGAAGAGCCCGAGGTAGATGTTTAACTTCCAGGCCACCTCAACCCAGAGGCTACT 1979
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 QY 2012 TATCTGAAGAGCCCGAGGTAGATGTTTAACTTCCAGGCCACCTCAACCCAGAGGCTACT 2071
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 QY 1980 CTGTGACTTAGACCTTACTGAAAGATCTCTGTCACTCACTGAAATTTCCAGGAACCA 2039
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 QY 2072 CTGTGACTTAGACCTTACTGAAAGATCTCTGTCACTCACTGAAATTTCCAGGAACCA 2131
 DB |||||
 QY 2040 AAAAGAGCA-CCCTATGGGCTTGGACCACTTACAGTGTGATAAGGCCTACTATACATTAG 2098
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 QY 2132 AAAAGAGCATCCCTATGGCTTGGACCACTTACAGTGTGATAAGGCCTACTATACATTAG 2191
 DB |||||
 QY 2099 GAAAGTGGAGTCTTTACTCGTCCCTTTTCATCGGTGCTGCTGCTGCTGCTGCTGCTGCTG 2158
 DB |||||
 QY 2192 GAAAGTGGAGTCTTTACTCGTCCCTTTTCATCGGTGCTGCTGCTGCTGCTGCTGCTGCTG 2251
 DB |||||
 QY 2159 TGGGTGGAGACTTTTCCATTAATCAATCAGGAATGAGTCAATCAGCCTTTTAGGTCTTT 2218
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 QY 2252 TGGGTGGAGACTTTTCCATTAATCAATCAGGAATGAGTCAATCAGCCTTTTAGGTCTTT 2311
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 QY 2219 AGTCCGGGGACTTGGGCTGAGAGAGTATAAATTAACCTTGGGCTGTCCAGCCTTTAATAG 2278
 DB |||||
 QY 2312 AGTCCGGGGACTTGGGCTGAGAGAGTATAAATTAACCTTGGGCTGTCCAGCCTTTAATAG 2370
 DB |||||
 QY 2279 ACTTCTTTACATTTTCTGCTGCTGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2338
 DB |||||
 QY 2371 ACTTCTTTACATTTTCTGCTGCTGAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2430
 DB |||||
 QY 2339 CCATCTCTGTAGGA 2352
 DB |||||
 QY 2431 CCATCTCTGTAGGA 2444

RESULT 4

US-09-840-989A-1
 ; Sequence 1, Application US/09840989A
 ; Patent No. US20020042372A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Olsen et al.
 ; TITLE OF INVENTION: Scannocalcin Polynucleotides, Polypeptides, and Methods Based The
 ; FILE REFERENCE: PF108P2
 ; CURRENT APPLICATION NUMBER: US/09/840, 989A
 ; CURRENT FILING DATE: 2001-04-25
 ; PRIOR APPLICATION NUMBER: PCT/US00/29432
 ; PRIOR FILING DATE: 2000-10-26

PRIOR APPLICATION NUMBER: US 60/161,740
PRIOR FILING DATE: 1999-10-27
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 1283
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (45)..(788)
OTHER INFORMATION:
NAME/KEY: misc_feature
LOCATION: (857)..(857)
OTHER INFORMATION: n is equal to a, t, c, or g.
NAME/KEY: misc_feature
LOCATION: (1254)..(1254)
OTHER INFORMATION: n is equal to a, t, c, or g.
NAME/KEY: misc_feature
LOCATION: (1279)..(1279)
OTHER INFORMATION: n is equal to a, t, c, or g.
US-09-840-989A-1

Query Match 32.6%; Score 1226; DB 10; Length 1283;
Best Local Similarity 98.9%; Pred. No. 6.8e-315;
Matches 1254; Conservative 0; Mismatches 12; Indels 2; Gaps 2;

QY 132 AAAAAAAAAAACCACAACTTAGCGGAAACTTCTCAGAGAATGCTCCAAAACCTCAGCA 191
DB 3 AAAAAAAAAAACCACAACTTAGCGGAAACTTCTCAGAGAATGCTCCAAAACCTCAGCA 62

QY 192 GTGCTTCTGGTGTGTGATCAGTGTCTCTGCAACCCATCAGCGGAGCAGAACTGACTCT 251
DB 63 GTGCTTCTGGTGTGTGATCAGTGTCTCTGCAACCCATCAGCGGAGCAGAACTGACTCT 122

QY 252 GTGAGCCCGAGGAAATCCGAGTGGCGGCTCAAACTCAGCTGAACTGTTGCTGCTC 311
DB 123 GTGAGCCCGAGGAAATCCGAGTGGCGGCTCAAACTCAGCTGAACTGTTGCTGCTC 182

QY 312 AACAGTGTCTACAGTCTGGCTCGGGGCTTTTGCATGCTGGAATCTCCACCTGTGAC 371
DB 183 AACAGTGTCTACAGTCTGGCTCGGGGCTTTTGCATGCTGGAATCTCCACCTGTGAC 242

QY 372 ACAGATGGATGATGACATCTGTAATCTTCTGTACAGCGCTCTAAATTTGACACT 431
DB 243 ACAGATGGATGATGACATCTGTAATCTTCTGTACAGCGCTCTAAATTTGACACT 302

QY 432 CAGGGAAGACATCTCTCAAGAGAGCTTAAATGTCATGCCAACGGGTCACTCCAG 491
DB 303 CAGGGAAGACATCTCTCAAGAGAGCTTAAATGTCATGCCAACGGGTCACTCCAG 362

QY 492 GTCTTCTCGCCATTCGGAGGTCTCCACTTTTCCAAAGGATGATTCCTGAGGTGCAGGAA 551
DB 363 GTCTTCTCGCCATTCGGAGGTCTCCACTTTTCCAAAGGATGATTCCTGAGGTGCAGGAA 422

QY 552 GAGTGTACAGCAAGTGAATGTGTCCAGATGCGCAAGCGGAACCTTGAAGCCATCACT 611
DB 423 GAGTGTACAGCAAGTGAATGTGTCCAGATGCGCAAGCGGAACCTTGAAGCCATCACT 482

QY 612 GAGTGTCTCAGTGTCCCAATCACTTCTCCACAGATACATATAACAGACTTGTCCGAAGC 671
DB 483 GAGTGTCTCAGTGTCCCAATCACTTCTCCACAGATACATATAACAGACTTGTCCGAAGC 542

QY 672 CTGCTGGAATGTGATGAAGACAGTCAGCACATCAGACAGCGCTGATGAGAAAT 731
DB 543 CTGCTGGAATGTGATGAAGACAGTCAGCACATCAGACAGCGCTGATGAGAAAT 602

QY 732 GGGCTTAACATGGCCAGCTCTTCCACATCTCTGACAGACAGCACTGTGCCCAACACAC 791
DB 603 GGGCTTAACATGGCCAGCTCTTCCACATCTCTGACAGACAGCACTGTGCCCAACACAC 662

QY 792 CCACGAGCTGACTTCAACAGGAGACGCCAATGAGCCGAGAGCTGAAAGTCTCTCTC 851

DB 663 CCACGAGCTGACTTCAACAGGAGACGCCAATGAGCCGAGAGCTGAAAGTCTCTCTC 722

QY 852 AGGAACCTCCGAGGTGAGGAGGACTCTCCCTCCCATCAAAACGACATCCCATGAGAGT 911

DB 723 AGGAACCTCCGAGGTGAGGAGGACTCTCCCTCCCATCAAAACGACATCCCATGAGAGT 782

QY 912 GCATAACACGAGGAGGTTATTACAACTCACCACAACTAGTATCATTTTAGGGGTGTTG 971

DB 783 GCATAACACGAGGAGGTTATTACAACTCACCACAACTAGTATCATTTTAGGGGTGTTG 842

QY 972 ACACACCGAGTTTGTAGTGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1031

DB 843 ACACACCGAGTTTGTAGTGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 902

QY 1032 TATCCCTTAAAGAAATTTGCATGAAACTAGGCTTCTGTAATCAATATCCCAACATTTCT 1091

DB 903 TATCCCTTAAAGAAATTTGCATGAAACTAGGCTTCTGTAATCAATATCCCAACATTTCT 962

QY 1092 GCAATGGAGCATTCCTCCACCAAAATCCATGTGACCATTCCTGCTCTCTCCTCAGGAGAA 1151

DB 963 GCAATGGAGCATTCCTCCACCAAAATCCATGTGACCATTCCTGCTCTCTCCTCAGGAGAA 1022

QY 1152 AGTACCTCTCTTACCAACTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1210

DB 1023 AGTACCTCTCTTACCAACTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1082

QY 1211 CCCAAACACAAACATTCATGTAATCTCCAGCCATTTGTAATTTGAAGATGCGATCCCT 1270

DB 1083 CCCAAACACAAACATTCATGTAATCTCCAGCCATTTGTAATTTGAAGATGCGATCCCT 1142

QY 1271 TTAG-AAGCGTTGCCCCAGTAGAGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGT 1329

DB 1143 TTAGAAACGGTTGCCCCAGTAGAGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGT 1202

QY 1330 TAAATGCTCATAAAGATGTTAAATGGAATTCGTTTATGAAATCTGCTGCTGCGCATGGAGC 1389

DB 1203 TAAATGCTCATAAAGATGTTAAATGGAATTCGTTTATGAAATCTGCTGCTGCGCATGGAGC 1262

QY 1390 AATATGAA 1397

DB 1263 AAAAAAAA 1270

RESULT 5
US-10-116-051-1
; Sequence 1, Application US/10116051
; Patent No. US20020146791A1
; GENERAL INFORMATION:
; APPLICANT: Olsen et al.
; TITLE OF INVENTION: CORPUSCLES OF STANNIUS PROTEIN, STANNIOCALCIN
; FILE REFERENCE: PF108P1D1C1
; CURRENT APPLICATION NUMBER: US/10/116,051
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 09/312,610
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 08/431,117
; PRIOR FILING DATE: 1995-04-28
; PRIOR APPLICATION NUMBER: 08/208,005
; PRIOR FILING DATE: 1994-03-08
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 771
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-116-051-1

Query Match 20.5%; Score 769.4; DB 12; Length 771;
Best Local Similarity 99.9%; Pred. No. 7.1e-194;
Matches 770; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 159 GAACTTCTCAGAGAAATGCTCCAAAACCTCAGCAGTGTCTTCTGGTGTGATCAGTGTCT 218


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; LENGTH: 585
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 10, 30, 32, 527, 565
; OTHER INFORMATION: n = A,T,C or G
US-09-910-689-149

Query Match      14.7%; Score 552; DB 10; Length 585;
Best Local Similarity 96.6%; Pred. No. 3.7e-136;
Matches 561; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 407 GTACAGCGCTGCTAAATTTGACACTCAGGGAAGCAATTCGTCAAAGAGAGCTTAAATG 466
Db 5 GTACANCACTGCTAAATTTGACACTNANGGAAAGCAATTCGTCAAAGAGAGCTTAAATG 64
QY 467 CATCGCCAAACGGGTGCTCAAGGTCTTCCTCGCCATTCGGAGGTGCTCCACATTTCCA 526
Db 65 CATCGCCAAACGGGTGCTCAAGGTCTTCCTCGCCATTCGGAGGTGCTCCACATTTCCA 124
QY 527 AAGGATGATTTGCTGAGGTGCGAGGAGGTGCTACAGCAAGCTGAATGTGTGCGAGCATCG 586
Db 125 AAGGATGATTTGCTGAGGTGCGAGGAGGTGCTACAGCAAGCTGAATGTGTGCGAGCATCG 184
QY 587 CAAGCGGAACCTGTAAGCCATCACTCAGGTGCTGCGAGGTGCTCCCAATCACTTCTCCAACAG 646
Db 185 CAAGCGGAACCTGTAAGCCATCACTCAGGTGCTGCGAGGTGCTCCCAATCACTTCTCCAACAG 244
QY 647 ATACTATACAGACTTGTCCGAAGCTGCTGGAATGTGATGAAGACACAGTCAGCACAAAT 706
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QY 707 CAGAGACAGCTGATGGAGAAATTTGGGCTTAACATGGCCAGCTCTTCCACATCTGCA 766
Db 305 CAGAGACAGCTGATGGAGAAATTTGGGCTTAACATGGCCAGCTCTTCCACATCTGCA 364
QY 767 GACAGACCACTGTGCCAAACACACCCACGAGCTGACTTCAACAGGAGACGCCCAATGA 826
Db 365 GACAGACCACTGTGCCAAACACACCCACGAGCTGACTTCAACAGGAGACGCCCAATGA 424
QY 827 GCCGAGAGAGCTGAAAGTCTCTCCAGGAACCTCCGAGGTGAGGAGTCTCCCTCCA 886
Db 425 GCCGAGAGAGCTGAAAGTCTCTCCAGGAACCTCCGAGGTGAGGAGTCTCCCTCCA 484
QY 887 CATCAACGCACTCCATCAGAGTGCATAACCCAGGAGAGGTTATTCAACACCTCCCA 946
Db 485 CATCAACGCACTCCATCAGAGTGCATAACCCAGGAGAGGTTATTCAACACCTCCCA 544
QY 947 AACTAGTATCATTTTAGGGGTGTTGACACACCAAGTTTGGAG 987
Db 545 ACTAGTATCATTTTAGGGGNGTTGACACACCAAGTTTGGAG 585

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RESULT 8

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US-10-010-742-149
; Sequence 149, Application US/10010742
; Patent No. US20020146727A1
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Day, Craig H.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Wang, Tongtong
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Bennington, Angela Ann
; APPLICANT: Zehentner, Barbara
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER

```

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; FILE REFERENCE: 210121.491C7
; CURRENT APPLICATION NUMBER: US/10/010,742
; CURRENT FILING DATE: 2001-11-30
; NUMBER OF SEQ ID NOS: 307
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 149
; LENGTH: 585
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 10, 30, 32, 527, 565
; OTHER INFORMATION: n = A,T,C or G
US-10-010-742-149

Query Match      14.7%; Score 552; DB 12; Length 585;
Best Local Similarity 96.6%; Pred. No. 3.7e-136;
Matches 561; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 407 GTACAGCGCTGCTAAATTTGACACTCAGGGAAGCAATTCGTCAAAGAGAGCTTAAATG 466
Db 5 GTACANCACTGCTAAATTTGACACTNANGGAAAGCAATTCGTCAAAGAGAGCTTAAATG 64
QY 467 CATCGCCAAACGGGTGCTCAAGGTCTTCCTCGCCATTCGGAGGTGCTCCACATTTCCA 526
Db 65 CATCGCCAAACGGGTGCTCAAGGTCTTCCTCGCCATTCGGAGGTGCTCCACATTTCCA 124
QY 527 AAGGATGATTTGCTGAGGTGCGAGGAGGTGCTACAGCAAGCTGAATGTGTGCGAGCATCG 586
Db 125 AAGGATGATTTGCTGAGGTGCGAGGAGGTGCTACAGCAAGCTGAATGTGTGCGAGCATCG 184
QY 587 CAAGCGGAACCTGTAAGCCATCACTCAGGTGCTGCGAGGTGCTCCCAATCACTTCTCCAACAG 646
Db 185 CAAGCGGAACCTGTAAGCCATCACTCAGGTGCTGCGAGGTGCTCCCAATCACTTCTCCAACAG 244
QY 647 ATACTATACAGACTTGTCCGAAGCTGCTGGAATGTGATGAAGACACAGTCAGCACAAAT 706
Db 245 ATACTATACAGACTTGTCCGAAGCTGCTGGAATGTGATGAAGACACAGTCAGCACAAAT 304
QY 707 CAGAGACAGCTGATGGAGAAATTTGGGCTTAACATGGCCAGCTCTTCCACATCTGCA 766
Db 305 CAGAGACAGCTGATGGAGAAATTTGGGCTTAACATGGCCAGCTCTTCCACATCTGCA 364
QY 767 GACAGACCACTGTGCCAAACACACCCACGAGCTGACTTCAACAGGAGACGCCCAATGA 826
Db 365 GACAGACCACTGTGCCAAACACACCCACGAGCTGACTTCAACAGGAGACGCCCAATGA 424
QY 827 GCCGAGAGAGCTGAAAGTCTCTCCAGGAACCTCCGAGGTGAGGAGTCTCCCTCCA 886
Db 425 GCCGAGAGAGCTGAAAGTCTCTCCAGGAACCTCCGAGGTGAGGAGTCTCCCTCCA 484
QY 887 CATCAACGCACTCCATCAGAGTGCATAACCCAGGAGAGGTTATTCAACACCTCCCA 946
Db 485 CATCAACGCACTCCATCAGAGTGCATAACCCAGGAGAGGTTATTCAACACCTCCCA 544
QY 947 AACTAGTATCATTTTAGGGGTGTTGACACACCAAGTTTGGAG 987
Db 545 ACTAGTATCATTTTAGGGGNGTTGACACACCAAGTTTGGAG 585

```

RESULT 9

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US-09-736-457-4/c
; Sequence 4, Application US/09736457
; Patent No. US20020168637A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedwick, Tom
; APPLICANT: Carter, Darriek
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane

```

```

; APPLICANT: Fan, Liqun
; APPLICANT: Wang, Aijun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C15
; CURRENT APPLICATION NUMBER: US/09/736,457
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 1864
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 510
; TYPE: DNA
; ORGANISM: Homo sapien
; US-09-736-457-4

Query Match      12.8%; Score 482.4; DB 9; Length 510;
Best Local Similarity 99.4%; Pred. No. 1.1e-117; Indels 2; Gaps 2;
Matches 505; Conservative 0; Mismatches 11;

QY 1578 AACTGCTCAGAGCTTTTAAAGTATCTTTTAAACAAATGCTTTTAAACCCAGAGAAATCTTTAAGG 1637
DB 508 AACTGCTCAGAGCTTTTAAAGTATCTTTTAAACAAATGCTTTTAAACCCAGAGAAATCTTTAAGG 449
QY 1638 TCTAAC-TGTGGAATATAATAGCTGAAACCTAATGCTACTGTACATAAATTTCCAGAGGAC 1696
DB 448 TCTAACCTTGTGGAATATAATAGCTGAAACCTAATGCTACTGTACATAAATTTCCAGAGGAC 389
QY 1697 TCTGCTTTAAACAAAGCAGTATATAAATCTTTTATTCATATAGATTTAGTTTGTAACTT 1756
DB 388 TCTGCTTTAAACAAAGCAGTATATAAATCTTTTATTCATATAGATTTAGTTTGTAACTT 329
QY 1757 AGCTTTATTTTCTTTTCTCGGAAATGGAATACTATCTCACTTCCAGATATCCACATAA 1816
DB 328 AGCTTTATTTTCTTTTCTCGGAAATGGAATACTATCTCACTTCCAGATATCCACATAA 269
QY 1817 ATGCTCCTTGTGGCCCTTTTATACTAAGGGGTAGAGTAGTTTAAATTCACATCAA 1876
DB 268 ATGCTCCTTGTGGCCCTTTTATACTAAGGGGTAGAGTAGTTTAAATTCACATCAA 209
QY 1877 AACTTAAGATGGCCCTGTATGACAGAGGAAACCAACAGGTTTATCTGAAGAGCCCGAG 1936
DB 208 AACTTAAGATGGCCCTGTATGACAGAGGAAACCAACAGGTTTATCTGAAGAGCCCGAG 149
QY 1937 GTAAGATGTTAATCTCCAGCCACCTCAACCCAGAGGCTACTCTTGACTTAGACCTATA 1996
DB 148 GTAAGATGTTAATCTCCAGCCACCTCAACCCAGAGGCTACTCTTGACTTAGACCTATA 89
QY 1997 CTGAAGATCTCTGTACATCCAACTGGAATTCAGGAAATCCAGGAAACCAAAAGAGCA-CCCTATG 2055
DB 88 CTGAAGATCTCTGTACATCCAACTGGAATTCAGGAAATTCAGGAAACCAAAAGAGCATCCCTATG 29
QY 2056 GCCTTGGACCACTTACAGTGTGATAAGG 2083
DB 28 GCCTTGGACCACTTACAGTGTGATAAGG 1

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RESULT 10
US-09-902-941-4/c
; Sequence 4, Application US/09902941
; Patent No. US2002017252A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, Robert A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Johnson, Jeffrey C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Marnerakis, Margarita
; APPLICANT: Carter, Darrick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: McNabb, Andria
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

```

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; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C17
; CURRENT APPLICATION NUMBER: US/09/902,941
; CURRENT FILING DATE: 2001-07-10
; NUMBER OF SEQ ID NOS: 2002
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 510
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-902-941-4

Query Match      12.8%; Score 482.4; DB 9; Length 510;
Best Local Similarity 99.4%; Pred. No. 1.1e-117; Indels 2; Gaps 2;
Matches 505; Conservative 1; Mismatches 11;

QY 1578 AACTGCTCAGAGCTTTTAAAGTATCTTTTAAACAAATGCTTTTAAACCCAGAGAAATCTTTAAGG 1637
DB 508 AACTGCTCAGAGCTTTTAAAGTATCTTTTAAACAAATGCTTTTAAACCCAGAGAAATCTTTAAGG 449
QY 1638 TCTAAC-TGTGGAATATAATAGCTGAAACCTAATGCTACTGTACATAAATTTCCAGAGGAC 1696
DB 448 TCTAACCTTGTGGAATATAATAGCTGAAACCTAATGCTACTGTACATAAATTTCCAGAGGAC 389
QY 1697 TCTGCTTTAAACAAAGCAGTATATAAATCTTTTATTCATATAGATTTAGTTTGTAACTT 1756
DB 388 TCTGCTTTAAACAAAGCAGTATATAAATCTTTTATTCATATAGATTTAGTTTGTAACTT 329
QY 1757 AGCTTTATTTTCTTTTCTCGGAAATGGAATACTATCTCACTTCCAGATATCCACATAA 1816
DB 328 AGCTTTATTTTCTTTTCTCGGAAATGGAATACTATCTCACTTCCAGATATCCACATAA 269
QY 1817 ATGCTCCTTGTGGCCCTTTTATACTAAGGGGTAGAGTAGTTTAAATTCACATCAA 1876
DB 268 ATGCTCCTTGTGGCCCTTTTATACTAAGGGGTAGAGTAGTTTAAATTCACATCAA 209
QY 1877 AACTTAAGATGGCCCTGTATGACAGAGGAAACCAACAGGTTTATCTGAAGAGCCCGAG 1936
DB 208 AACTTAAGATGGCCCTGTATGACAGAGGAAACCAACAGGTTTATCTGAAGAGCCCGAG 149
QY 1937 GTAAGATGTTAATCTCCAGCCACCTCAACCCAGAGGCTACTCTTGACTTAGACCTATA 1996
DB 148 GTAAGATGTTAATCTCCAGCCACCTCAACCCAGAGGCTACTCTTGACTTAGACCTATA 89
QY 1997 CTGAAGATCTCTGTACATCCAACTGGAATTCAGGAAATTCAGGAAACCAAAAGAGCA-CCCTATG 2055
DB 88 CTGAAGATCTCTGTACATCCAACTGGAATTCAGGAAATTCAGGAAACCAAAAGAGCATCCCTATG 29
QY 2056 GCCTTGGACCACTTACAGTGTGATAAGG 2083
DB 28 GCCTTGGACCACTTACAGTGTGATAAGG 1

RESULT 11
US-09-849-626-4/c
; Sequence 4, Application US/09849626
; Publication No. US20020197669A1
; GENERAL INFORMATION:
; APPLICANT: Bangur, Chaitanya
; APPLICANT: Fanger, Gary
; APPLICANT: Wang, Aijun
; APPLICANT: Wang, Tongtong
; APPLICANT: Switzer, Anne
; APPLICANT: McNeill, Patricia
; APPLICANT: Clapper, Jonathan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C16
; CURRENT APPLICATION NUMBER: US/09/849,626
; CURRENT FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 1926
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4

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; LENGTH: 510
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-849-626-4

Query Match      12.8%; Score 482.4; DB 9; Length 510;
Best Local Similarity 99.4%; Pred. No. 1.1e-117;
Matches 505; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

QY 1578 AACTGCTCAGAGCTTTTAAAGTATCTTTAAACAAATGCTTTAAACCCAGAGAATCTTAAAGG 1637
Db      |||||||
QY 508 AACTGCTCAGAGCTTTTAAAGTATCTTTAAACAAATGCTTTAAACCCAGAGAATCTTAAAGG 449
Db      |||||||
QY 1638 TCTAAC-TGTGGAATATAAATAGCTGAAACCTAATGCTGTACATATAAATTCAGAGGAC 1696
Db      |||||||
QY 448 TCTAAC-TGTGGAATATAAATAGCTGAAACCTAATGCTGTACATATAAATTCAGAGGAC 389
Db      |||||||
QY 1697 TCTGCTTTAAACAAAGCAGTATATAAATCTTTTATTCATATAGATTTAGTTTGAACCTT 1756
Db      |||||||
QY 388 TCTGCTTTAAACAAAGCAGTATATAAATCTTTTATTCATATAGATTTAGTTTGAACCTT 329
Db      |||||||
QY 1757 AGCTTTATTTTCTTTTCTGCGGAAATGGAATTAATCTTCACTTCCAGATATCCACATAA 1816
Db      |||||||
QY 328 AGCTTTATTTTCTTTTCTGCGGAAATGGAATTAATCTTCACTTCCAGATATCCACATAA 269
Db      |||||||
QY 1817 ATGCTCCTTGTGGCCCTTTTATAAATAAGGGGTAGAGTAGTTTAAATTCACATCAA 1876
Db      |||||||
QY 268 ATGCTCCTTGTGGCCCTTTTATAAATAAGGGGTAGAGTAGTTTAAATTCACATCAA 209
Db      |||||||
QY 1877 AACTTAAGATGGCCCTGTATGACAGAGGAAACCAACAGGTTTATCTCAAGGACCCAG 1936
Db      |||||||
QY 208 AACTTAAGATGGCCCTGTATGACAGAGGAAACCAACAGGTTTATCTCAAGGACCCAG 149
Db      |||||||
QY 1937 GTAAGATGTTAATCTCCAGCCCACTCAACCCAGAGGCTACTCTTGACTTAGACCTATA 1996
Db      |||||||
QY 148 GTAAGATGTTAATCTCCAGCCCACTCAACCCAGAGGCTACTCTTGACTTAGACCTATA 89
Db      |||||||
QY 1997 CTGAAGATCTCTGTCCACATCCAATCGGAAATTCAGGAAACCAAAAGAGCA-CCCTATG 2055
Db      |||||||
QY 88 CTGAAGATCTCTGTCCACATCCAATCGGAAATTCAGGAAACCAAAAGAGCATCCCTATG 29
Db      |||||||
QY 2056 GCCTTGGACCACTTACAGTGTGATAAGG 2083
Db      |||||||
QY 28 GCCTTGGACCACTTACAGTGTGATAAGG 1

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RESULT 12
US-10-017-754-4/c
; Sequence 4, Application US/10017754
; Publication No. US20030054363A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, Robert A.
; APPLICANT: Wang, Tonglong
; APPLICANT: Watanabe, Yoshihito
; APPLICANT: Johnson, Jeffrey C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Marnerakis, Margarita
; APPLICANT: Carter, Darrick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: McNabb, Andria
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.478C18
; CURRENT APPLICATION NUMBER: US/10/017,754
; CURRENT FILING DATE: 2001-10-29
; NUMBER OF SEQ ID NOS: 2004
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 510
; TYPE: DNA
; ORGANISM: Homo sapiens

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```

US-10-017-754-4

Query Match      12.8%; Score 482.4; DB 9; Length 510;
Best Local Similarity 99.4%; Pred. No. 1.1e-117;
Matches 505; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

QY 1578 AACTGCTCAGAGCTTTTAAAGTATCTTTAAACAAATGCTTTAAACCCAGAGAATCTTAAAGG 1637
Db      |||||||
QY 508 AACTGCTCAGAGCTTTTAAAGTATCTTTAAACAAATGCTTTAAACCCAGAGAATCTTAAAGG 449
Db      |||||||
QY 1638 TCTAAC-TGTGGAATATAAATAGCTGAAACCTAATGCTGTACATATAAATTCAGAGGAC 1696
Db      |||||||
QY 448 TCTAAC-TGTGGAATATAAATAGCTGAAACCTAATGCTGTACATATAAATTCAGAGGAC 389
Db      |||||||
QY 1697 TCTGCTTTAAACAAAGCAGTATATAAATCTTTTATTCATATAGATTTAGTTTGAACCTT 1756
Db      |||||||
QY 388 TCTGCTTTAAACAAAGCAGTATATAAATCTTTTATTCATATAGATTTAGTTTGAACCTT 329
Db      |||||||
QY 1757 AGCTTTATTTTCTTTTCTGCGGAAATGGAATTAATCTTCACTTCCAGATATCCACATAA 1816
Db      |||||||
QY 328 AGCTTTATTTTCTTTTCTGCGGAAATGGAATTAATCTTCACTTCCAGATATCCACATAA 269
Db      |||||||
QY 1817 ATGCTCCTTGTGGCCCTTTTATAAATAAGGGGTAGAGTAGTTTAAATTCACATCAA 1876
Db      |||||||
QY 268 ATGCTCCTTGTGGCCCTTTTATAAATAAGGGGTAGAGTAGTTTAAATTCACATCAA 209
Db      |||||||
QY 1877 AACTTAAGATGGCCCTGTATGACAGAGGAAACCAACAGGTTTATCTCAAGGACCCAG 1936
Db      |||||||
QY 208 AACTTAAGATGGCCCTGTATGACAGAGGAAACCAACAGGTTTATCTCAAGGACCCAG 149
Db      |||||||
QY 1937 GTAAGATGTTAATCTCCAGCCCACTCAACCCAGAGGCTACTCTTGACTTAGACCTATA 1996
Db      |||||||
QY 148 GTAAGATGTTAATCTCCAGCCCACTCAACCCAGAGGCTACTCTTGACTTAGACCTATA 89
Db      |||||||
QY 1997 CTGAAGATCTCTGTCCACATCCAATCGGAAATTCAGGAAACCAAAAGAGCA-CCCTATG 2055
Db      |||||||
QY 88 CTGAAGATCTCTGTCCACATCCAATCGGAAATTCAGGAAATTCAGGAAACCAAAAGAGCATCCCTATG 29
Db      |||||||
QY 2056 GCCTTGGACCACTTACAGTGTGATAAGG 2083
Db      |||||||
QY 28 GCCTTGGACCACTTACAGTGTGATAAGG 1

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RESULT 13
US-10-060-036-2677/c
; Sequence 2677, Application US/10060036
; Publication No. US20030073144A1
; GENERAL INFORMATION:
; APPLICANT: Benson, Darin R.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Persing, David H.
; APPLICANT: Hepler, William T.
; APPLICANT: Jiang, Yudi
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.565
; CURRENT APPLICATION NUMBER: US/10/060,036
; CURRENT FILING DATE: 2002-01-30
; NUMBER OF SEQ ID NOS: 4560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2677
; LENGTH: 473
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-036-2677

Query Match      12.5%; Score 471.4; DB 9; Length 473;
Best Local Similarity 99.8%; Pred. No. 8.4e-115;
Matches 472; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 518 CACTTCCAAAGGATGATTGCTGAGGTGCAAGAGTGTACAGCAAGCTGAATGTGTG 577

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Db 473 CACTTCCAAAGGATGATGCTGAGGTGAGGAGAGTGCTACAGCAAGCTGAATGTG 414
QY 578 CAGCATCGCAAGCGAACCTTGAAGCCATCACTGAGGTGCTCCAGCTGCCCAATCACTT 637
Db 413 CAGCATCGCAAGCGAACCTTGAAGCCATCACTGAGGTGCTCCAGCTGCCCAATCACTT 354
QY 638 CTCGAACAGATATAACAGACTTGTCCGAAGCTGTGGAATGTGATGAAGACACAGT 697
Db 353 CTCGAACAGATATAACAGACTTGTCCGAAGCTGTGGAATGTGATGAAGACACAGT 294
QY 698 CAGCAACATCAGAGACAGCTGTGAGAAATTTGGCCCTTAACATGCCAGCTCTTCCA 757
Db 293 CAGCAACATCAGAGACAGCTGTGAGAAATTTGGCCCTTAACATGCCAGCTCTTCCA 234
QY 758 CATCTTCGACAGACAGCTGTGCCCAACACACACCCAGAGCTGACTTCAACAGGAGAG 817
Db 233 CATCTTCGACAGACAGCTGTGCCCAACACACACCCAGAGCTGACTTCAACAGGAGAG 174
QY 818 CACCAATGAGCGCAGAAAGCTGAAAGTCTCTTCAGGAACTCCGAGGTGAGGAGGACTC 877
Db 173 CACCAATGAGCGCAGAAAGCTGAAAGTCTCTTCAGGAACTCCGAGGTGAGGAGGACTC 114
QY 878 TCCTCTCCACATCAAAAGCAGACATCCCATGAGGTGATACACAGGAGAGGTTATTCA 937
Db 113 TCCTCTCCACATCAAAAGCAGACATCCCATGAGGTGATACACAGGAGAGGTTATTCA 54
QY 938 ACCTCACCAAACTAGTATCATTTAGGGGTGTTGACACACCACTTTTGAGTGT 990
Db 53 ACCTCACCAAACTAGTATCATTTAGGGGTGTTGACACACCACTTTTGAGTGT 1

RESULT 14
US-09-918-995-33032
; Sequence 33032, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 33032
; LENGTH: 436
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-995-33032

Query Match
Best Local Similarity 11.6%; Score 436; DB 9; Length 436;
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 686 TGAAGACACAGTCAGCACATCAGACAGCCTGTGAGGAAATTTGGCCCTTAACATGCG 745
Db 1 TGAAGACACAGTCAGCACATCAGACAGCCTGTGAGGAAATTTGGCCCTTAACATGCG 60
QY 746 CAGCCTCTTCCATCCTCGACAGACACCACTGTGCCCAACACACACCCAGAGCTGACTT 805
Db 61 CAGCCTCTTCCATCCTCGACAGACACCACTGTGCCCAACACACACCCAGAGCTGACTT 120
QY 806 CACAGGAGACCGCAATGAGCGCAGAGCTGAAGTCTCTCCTCAGGAACTCCGAGG 865
Db 121 CACAGGAGACCGCAATGAGCGCAGAGCTGAAGTCTCTCCTCAGGAACTCCGAGG 180
QY 866 TGAGGAGGACTCTCTCTCCCATCAATCAAAAGCAGACATCCCATGAGGTGATGAACACAGGAG 925
Db 181 TGAGGAGGACTCTCTCTCCCATCAATCAAAAGCAGACATCCCATGAGGTGATGAACACAGGAG 240
QY 926 AGGTTATTCACAACTTCACAAACTAGTATCATTTTAGGGGTGTTGACACACCAAGTTTGTG 985

Db 241 AGGTTATTCACAACTTCACAAACTAGTATCATTTTAGGGGTGTTGACACACCAAGTTTGTG 300
QY 986 AGTGTACTGTGCTCGTGGTTTGAATTTTAAAGTAGTCTCTATTTTCTATCCCCCTTAAAG 1045
Db 301 AGTGTACTGTGCTCGTGGTTTGAATTTTAAAGTAGTCTCTATTTTCTATCCCCCTTAAAG 360
QY 1046 AAAATTTGCATGAACTAGGCTTCTGTAATCAATATCCCAACATTTCTGCAATGGCAGCAT 1105
Db 361 AAAATTTGCATGAACTAGGCTTCTGTAATCAATATCCCAACATTTCTGCAATGGCAGCAT 420
QY 1106 CCCACCAACAAATCC 1121
Db 421 CCCACCAACAAATCC 436

RESULT 15
US-09-778-320-141
; Sequence 141, Application US/09778320
; Patent No. US20010034052A1
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Day, Craig H.
; APPLICANT: Jiang, Yugu
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Wang, TongTong
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.491C5
; CURRENT APPLICATION NUMBER: US/09/778,320
; CURRENT FILING DATE: 2001-02-06
; NUMBER OF SEQ ID NOS: 301
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 141
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(420)
; OTHER INFORMATION: n = A,T,C or G
US-09-778-320-141

Query Match
Best Local Similarity 8.5%; Score 320; DB 10; Length 420;
Matches 379; Conservative 0; Mismatches 25; Indels 6; Gaps 5;

QY 426 GACACTCAGGGAAGAACATTCGTCAAAGAGAGCTTAAATGATCGCCCAACCGGGTCACC 485
Db 1 GACACTCAGGGAAGAACATTCGTCAAAGAGAGCTTAAATGATCGCCCAACCGGGTCACC 60
QY 486 TCCAAAGGTCTTCCTCGCCATTCGGAGGTGCTCCATTTCCAAAGGATGATGCTGAGGTG 545
Db 61 TCCAAAGGTCTTCCTCGCCATTCGGAGGTGCTCCATTTCCAAAGGATGATGCTGAGGTG 120
QY 546 CAGGAAGAGTCTCAGCAAGCTGAATGTGTCAGCAGCTGCCAAGCGGAACCTCGAAGC 605
Db 121 CAGGAAGAGTCTCAGCAAGCTGAATGTGTCAGCAGCTGCCAAGCGGAACCTCGAAGC 180
QY 606 ATCACTGAGGTGCTCCAGCTGCCAATCACTTCTCCAAAGATCTATAAAGAGCTTTGTC 665
Db 181 ATCACTGAGGTGCTCCAGCTGCCAATCACTTCTCCAAAGATCTATAAAGAGCTTTGNN 240
QY 666 CGAAGCTCTGGAATGTGATGAAGACACA-GTACGACAAATCA-GAGACAGCTGATGG 723
Db 241 CGAAGCTCTGGAATGTGATGAAGACACAAGGAGGAGCAATCAGGAGACAGCTGATGG 300
QY 724 AGAAATTTGGGCTTAACATGGCCA-GCCTCTTTCCACATCTCTG--CAGACAGACCACTGTG 780
Db 301 ANAAANTGGGCTTANCAATGTCAGGCTCTTTCCACATCTCTTNGANGACAGACCACTGTG 360

Qy 781 CCGAACAACACCCAC-GAGCTGACTTCAACAGGAGAGCGCACCAATGAGCC 829
Db 361 CCGAACAACACCCCTGAGCTGACTTNNACAGGAGAGCGCACNAAGGAGCC 410

Search completed: June 9, 2003, 15:59:33
Job time : 488 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 12, 2003, 21:15:35 ; Search time 1994 Seconds
(without alignments)
3605.012 Million cell updates/sec

Title: US-09-705-500A-3
Perfect score: 247
Sequence: 1 MLQNSAVLLVLVISATHE.....NLRGEDSPSHIKRTSHESA 247

Scoring table: OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2054640 seqs, 14551402878 residues

Word size: 1

Total number of hits satisfying chosen parameters: 4106482

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Command line parameters:
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-UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cgi -LIST=1000
-DOCALIGN=200 -THR SCORE=quality -THR_MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc
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-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
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-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :

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41: em.htgo.other.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	DB ID	Description
1	247	100.0	741	6	E37712 Osteogenesi
2	247	100.0	741	6	E39295 Novel prote
3	247	100.0	771	6	AR055558 Sequence
4	247	100.0	771	6	AR051578 Sequence
5	247	100.0	840	9	HSU46768 Human stann
6	247	100.0	2481	9	BC029044 Homo sapi
7	247	100.0	3901	9	HSU25997 Homo sapien
8	160	64.8	585	6	AX156292 Sequence
9	90	36.4	18216	9	AF242179 Homo sapi
10	90	36.4	154898	9	AC012119 Homo sapi
11	86	34.8	834	4	AF257506 Bos tauru
12	84	34.0	1004	10	MMU62667 Rattus norv
13	84	34.0	1232	10	U47815 Mus musculu
14	84	34.0	2341	10	BC021425 Mus muscu
15	84	34.0	4183	10	AF099098 Mus muscu
16	75	30.4	177104	10	AC091237 Mus muscu
17	73	29.6	4479	9	AF098463 Homo sapi
18	40	16.2	420	6	AX156284 Sequence
19	17	6.9	314	11	G60515 SHCC-35548
20	15	6.1	2807	5	AB060558 Osteogios
21	14	5.7	555	5	S80134 Oncorhynch
22	14	5.7	1743	5	AF326317 Oncorhync
23	14	5.7	1850	5	AF326318 Oncorhync
24	14	5.7	1934	5	S59519 stanniocalc
25	12	4.9	2190	6	A05174 Synthetic n
26	12	4.9	2192	5	ANGCSPA
27	10	4.0	90019	8	TW021B04
28	9	3.6	227	8	AY023639 Oryza sat
29	9	3.6	436	6	AX309100 Sequence
30	9	3.6	647	5	TCA309137 Triturus
31	9	3.6	6440	3	AF040989 Drosophil
32	9	3.6	16652	2	AC014298 Drosophil
33	9	3.6	39104	6	AX059498 Sequence
34	9	3.6	81877	8	T32B20 Arabidops
35	9	3.6	88200	9	AC023061 Homo sapi
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39	9	3.6	96583	8	ATAC009992 Arabidops
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46	9	3.6	113578	2	AC019916 Drosophil
47	9	3.6	116416	2	AC130801 Medicago
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49	9	3.6	126087	8	AF147264 Arabidops
50	9	3.6	139848	10	AC122904 Mus muscu

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Db	361	ATTGCTGAGTGCAGGAAGAGTGTACAGCAAGCTGAATGTGTGACGATCCCAAGCGG	420
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QY	181	SerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp	200
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QY	201	HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgThrAsnGluProGln	220
Db	601	CACTGTGCCCAACACACCCAGAGTGTACTTCAACAGGAGAGCCACCAATGAGCGGAG	660
QY	221	LysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHisIleLys	240
Db	661	AAGCTGAAAGTCTCTCTAGGAACCTCCGAGGTGAGGAGTCTCTCCCTCCACATCAA	720
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DEFINITION			Novel protein and process for producing the same.
ACCESSION			E39295
VERSION			E39295.1 GI:18628926
KEYWORDS			JP 2000239299-A/12.
SOURCE			Homo sapiens.
ORGANISM			Homo sapiens
REFERENCE			
AUTHORS			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE			1 (bases 1 to 741)
JOURNAL			Goto, M., Tomoyasu, M., Yamaguchi, K., Kinoshita, M., Shima, N., Yasuda, N. and Nakagawa, N.
COMMENT			Novel protein and process for producing the same
			Patent: JP 2000239299-A 12 05-SEP-2000;
			SNOW BRAND MILK PROD CO LTD
			OS Homo sapiens (human)
			PN JP 2000239299-A/12
			PD 05-SEP-2000
			PF 13-FEB-1999 JP 1999036225
			PR MASAOKI GOTO, MASAOKI TOMOYASU, KYOJI YAMAGUCHI, PI MASAHIKO KINOZAKI,
			PI NOBUYUKI SHIMA, NAOTAKA YASUDA, NOBUAKI NAKAGAWA PC
			C07K14/47, C12N5/10, C12N15/09, C12P21/02//A61K31/00, A61K31/00, PC
			A61K38/00,
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Percent Similarity:	100.00%	Conservative:	0
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Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0

US-09-705-500A-3 (1-247) x E39295 (1-741)			
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Db	61	GCGAGCAGAAATGACTCTGTGAGCCCGAGAAATCCGAGTGGCGGCCCAAACTCAGCT	120
Qy	41	GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu	60
Db	121	GAAGTGGTTCGTGCTCAACAGTCTCTACAGTTCGGTGGCGGCTTTTGATCGCTG	180
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Qy	181	SerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp	200
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Qy	241	ArgThrSerHisGluSerAla	247
Db	721	CGCACATCCCATGAGAGTGCA	741
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AR055558			
LOCUS			
DEFINITION			
Sequence 1 from patent US 5837498.			
ACCESSION			
AR055558			
VERSION			
AR055558.1 GI:5981135			
KEYWORDS			
Unknown.			
SOURCE			
Unknown.			
ORGANISM			
Unclassified.			
REFERENCE			
1 (bases 1 to 771)			
AUTHORS			
Olsen, H.S. and Adams, M.D.			
TITLE			
Corpuscles of stannius protein, stannioalcin			
JOURNAL			
Patent: US 5837498-A 1 17-NOV-1998;			
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Location/Qualifiers			
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Db	455	AACCTTGAGGCCATCACTGAGGTGTCAGCTGCCCAATCATTCTTCCAAACATACTAT	514
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Qy	181	SerLeuMetGluIlystleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp	200
Db	575	AGCCTGATGAGAAAAATGGGCTAAATGATGGCCAGCTCTTCCACATCCTCGCAGACAGAC	634
Qy	201	HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgThrAsnGluProGln	220
Db	635	CACGTGTGCCNAACACACCCAGAGCTGACTTCACAGAGAGCCACCAATGAGCGCAG	694
Qy	221	LysLeuLysValLeuLeuArgAsnLeuArgGlyGluAspSerProSerHisIleLys	240
Db	695	AAGCTGAAAGTCTCTCTCAGGAACCTCCGAGGTGAGGAGGACTTCTCCCTCCACATCAA	754
Qy	241	ArgThrSerHisGluSerIle	247
Db	755	CGCACATCCCATGAGAGTGCA	775
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DEFINITION		Homo sapiens, stanniocalcin 1, clone MGC:34539 IMAGE:5191420, mRNA, complete cds.	
ACCESSION	BC029044		
VERSION	BC029044.1	GI:20810067	
KEYWORDS	MGC.		
SOURCE	Homo sapiens.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 2481)		
TITLE	Strausberg, R.		
JOURNAL	Direct Submission		
REMARK	Submitted (01-MAY-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA		
COMMENT	NIH-MGC Project URL: http://mgc.nci.nih.gov Contact: MGC help desk Email: cgapbs@mail.nih.gov Tissue Procurement: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center Center code: BCM-HGSC Web site: http://www.hgsc.bcm.tmc.edu/cdna/ Contact: ang@bcm.tmc.edu Gunnaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M., Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M., Richards, S., Gibbs, R.A.		
FEATURES	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 50 Row: k Column: 5 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4507264. Location/Qualifiers 1..2481 /organism="Homo sapiens" /db_xref="locusID:6781" /db_xref="taxon:9606" /clone="MGC:34539 IMAGE:5191420" /tissue type="Colon, Kidney, Stomach, adult, whole pooled"		
SOURCE			

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BASE COUNT      745 a      599 c      520 g      617 t
ORIGIN

Alignment Scores:
Pred. No.:      9,01e-274      Length:      2481
Score:      247.00      Matches:      247
Percent Similarity:      100.00%      Conservative:      0
Best Local Similarity:      100.00%      Mismatches:      0
Query Match:      100.00%      Indels:      0
DB:      3      Gaps:      0

US-09-705-500A-3 (1-247) x BC029044 (1-2481)

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QY      21. AlaGluGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
Db      323  GCGGAGCAGAAATGACTCTGTGAGCCCGAGAAATCCCGAGTGGCGGCTCAAAACTCAGCT 382
QY      41. GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
Db      383  GAAGTGGTTTCGTTGCCCTCAACAGTGCTCTACAGGTGGGCTCGCGGGCTTTGTCATGCTG 442
QY      61. GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
Db      443  GAAACTCCACTGTGACACAGATGGGATGTATGACATCTGTAAATCCTTCTGTGTACGC 502
QY      81. AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAla 100
Db      503  GCTGCTAAATTTGACACTCAGGGGAAAAGCATTCGTCAAAGAGAGAGCTTAAATAATGCATCG 562
QY      101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
Db      563  AACGGGGTCACCTCCAAAGGCTTCTCTCGCCATTGCGAGGTGCTCCACTTTCCAAAGGATG 622
QY      121 IleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
Db      623  ATTGCTGAGTGCAGGAAGAGTGTCTACAGCAAGCTGAATGTGTGACGATCGCCACGCGG 682
QY      141 AsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
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QY      161 AsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp 180
Db      743  AACAGACTTGTCCGAAGCCCTGCTGGAATGTGATGAAGACACAGTCAGCAGCAAAATCAGAC 802
QY      181 SerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
Db      803  AGCCTGATGAGAGAAATTTGGGCCCTTAAATGGCCAGCCCTCTTCCACATCTCTGCGACAG 862
QY      201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgThrAsnGluProGln 220
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DEFINITION	Homo sapiens stanniocalcin precursor (STC) mRNA,	linear	PRI 02-APR-1998
ACCESSION	U25997		
VERSION	U25997.1	GI:3006202	
KEYWORDS			
SOURCE	Homo sapiens.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	1 (bases 1 to 3901)		
JOURNAL	Chang,A.C., Janosi,J., Hulsbeek,M., de Jong,D., Jeffrey,K.J.,		
MEDLINE	Noble,J.R. and Reddel,R.R.		
PUBMED	A novel human cDNA highly homologous to the fish hormone		
REFERENCE	stanniocalcin		
AUTHORS	.Mol. Cell. Endocrinol. 112 (2), 241-247 (1995)		
TITLE	2 (bases 1 to 3901)		
JOURNAL	Chang,A.C., Jeffrey,K.J., Tokutake,Y., Shimamoto,A., Neumann,A.A.,		
MEDLINE	Dunham,M.A., Cha,J., Sugawara,M., Furuichi,Y. and Reddel,R.R.		
PUBMED	Hunan stanniocalcin (STC): genomic structure, chromosomal		
REFERENCE	localization, and the presence of CAG trinucleotide repeats		
AUTHORS	Genomics 47 (3), 393-398 (1998)		
TITLE	3 (bases 1 to 3901)		
JOURNAL	Chang,A.C.-W.		
MEDLINE	Direct Submission		
PUBMED	Submitted (02-MAY-1995) Childrens Medical Research Institute, 214		
REFERENCE	Hawkesbury Road, Westmead, NSW 2145, Australia		
AUTHORS	4 (bases 1 to 3901)		
TITLE	Chang,A.C.-W.		
JOURNAL	Direct Submission		
PUBMED	Submitted (02-APR-1998) Childrens Medical Research Institute, 214		
REFERENCE	Hawkesbury Road, Westmead, NSW 2145, Australia		
AUTHORS	Sequence update by submitter		
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AUTHORS	/product="stanniocalcin precursor"		
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AUTHORS	VTSKVLAIRGCSTFORMIAEVOECYSLKNVCYIAKRNPETAEVVQLPNHFSNRVY		
TITLE	NRLVRSLLCEDTDTVTRDSLMKXIKGIPNKWSLPHILQTDHCQATHPRADFNRRRTNE		
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PUBMED			

SOURCE	Homo sapiens.
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 18216)
AUTHORS	Jeffrey,K.J. and Reddel,R.R.
TITLE	Characterization of the human stanniocalcin 1 gene
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 18216)
AUTHORS	Jeffrey,K.J. and Reddel,R.R.
TITLE	Direct Submission
JOURNAL	Submitted (05-MAR-2000) Cancer Research Group, Children's Medical Research Institute, 214 Hawkesbury Road, Westmead, NSW 2145, Australia
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exon	4430. .4572
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Query Match:	36.44% Indels: 0
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US-09-705-500A-3 (1-247) x AF242179 (1-18216)	
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QY	198 GlnThrAspHisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgThrAsn 217
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Center code: WIBR
 Web site: http://www-seq.wi.mit.edu
 Contact: sequence_submissions@genome.wi.mit.edu
 ----- Project Information
 Center project name: L2190
 Center clone name: 175_E_9

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 Percent Similarity: 100.00% Conservative: 0
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QY 218 GluProGlnIlyLeuIlyValLeuLeuArgAsnLeuArgGluGluAspSerProSer 237
Db 54390 GAGCCCGAGAGCTGAAGTCTCTCTCAGAACCTCCGAGGTGAGGAGGACTCTCTCTCC 54449
QY 238 HisIleLysArgThrSerHisGluSerAla 247
Db 54450 CACATCAACGACATCCCATGAGAGTGCA 54479

RESULT 11
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LOCUS Bos taurus stanniocalcin mRNA, complete cds.
DEFINITION AF257506
ACCESSION AF257506
VERSION AF257506.1 GI:7739750
KEYWORDS Bos taurus.
SOURCE Bos taurus.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
1 (bases 1 to 834)
DiMattia,G.E.
TITLE bovine stanniocalcin cDNA sequence
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 834)
AUTHORS DiMattia,G.E.
DIRECT SUBMISSION
TITLE Submitted (18-APR-2000) Oncology, London Regional Cancer centre,
JOURNAL 790 Commissioners Rd., London, ON N6A 4L6, Canada
FEATURES
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Location/Qualifiers
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3'UTR
BASE COUNT 218 a 227 c 215 g 174 t
ORIGIN
Alignment Scores:
Pred. No.: 6,03e-89 Length: 834
Score: 86.00 Matches: 86
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 34.82% Indels: 0
DB: 4 Gaps: 0

US-09-705-500A-3 (1-247) x AF257506 (1-834)
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US-09-705-500A-3 (1-247) x AC012119 (1-154898)
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Db 54450 CACATCAACGACATCCCATGAGAGTGCA 54479

RESULT 12
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LOCUS Rattus norvegicus stanniocalcin (rSTC) mRNA, complete cds.
DEFINITION Rattus norvegicus stanniocalcin (rSTC) mRNA, complete cds.
ACCESSION RNU62667
VERSION U62667.1 GI:1762530
KEYWORDS Rattus norvegicus.
SOURCE Rattus norvegicus.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 1004)
Abe,T., Tanemoto,M., Hall,A.E., Brown,E.M. and Hebert,S.C.
TITLE Molecular cloning and characterization of rat stanniocalcin peptide
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1004)
AUTHORS Abe,T., Tanemoto,M., Hall,A.E., Brown,E.M. and Hebert,S.C.
DIRECT SUBMISSION
TITLE Submitted (01-JUL-1996) Renal Division, Brigham and Women's
JOURNAL Hospital, 75 Francis Street, Boston, MA 02115, USA
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Query Match: 34.01% Indels: 6
DB: 10 Gaps: 0

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ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 1232)
AUTHORS Chang,A.C., Dunham,M.A., Jeffrey,K.J. and Reddel,R.R.
TITLE Molecular cloning and characterization of mouse stanniocalcin cDNA
JOURNAL Mol. Cell. Endocrinol. 124 (1-2), 185-187 (1996)
MEDLINE 97179050
PUBMED 9027337
REFERENCE 2 (bases 1 to 1232)
AUTHORS Chang,A.C.M. and Reddel,R.R.
TITLE Direct Submission
JOURNAL Submitted (30-JAN-1996) Andy C.M. Chang, Cancer Research Group, Children's Medical Research Institute, 214 Hawkesbury Road, Westmead, Sydney, NSW 2145, Australia
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ACCESSION BC021425
VERSION BC021425.1 GI:19203894
KEYWORDS MGC.

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SOURCE house mouse.
ORGANISM Mus musculus
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AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE 1 (bases 1 to 2341)
JOURNAL Strausberg,R.
Direct Submission
Submitted (14-JAN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgabbs@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc.mgc@nih.gov
Contact: nisc.mgc@nih.gov
Akter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,
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Maduro, O.L., Masello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,
McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,
Tsurgou, C., Vogt, J.D., Walker, M.A., Wetherby, K.D., Wiggins, L.,
Young, A., Zhang, L.-H. and Green, E.D.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov
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VERSION AF099098.1 GI:3851659
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ORGANISM Mus musculus
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 4183)
AUTHORS Varghese, R., Wong, C.K.C., Doel, H., Wagner, G.F. and DiMattia, G.E.
TITLE Comparative Analysis of Mammalian Stanniocalcin Genes
JOURNAL Endocrinology 139, 4717-4725 (1998)
REFERENCE 2 (bases 1 to 4183)
AUTHORS DiMattia, G.E., Varghese, R. and Wagner, G.F.
TITLE Direct Submission
JOURNAL Submitted (16-OCT-1998) Oncology, London Regional Cancer Centre,
790 Commissioners Rd., London, ONT N6C 4L6, Canada
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GenCore version 5.1.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

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Run on: June 12, 2003, 21:14:10 ; Search time 223 Seconds
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Perfect score: 247

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SUMMARIES

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5	247	100.0	771	21	AAZ39520	Human corpuscles o
6	247	100.0	1283	22	AAF83297	Human stannocalci
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8	184	74.5	2572	21	AAF16051	Human prostate can
9	160	64.8	585	22	AAH55624	Human breast tumou
C 10	72	29.1	219	22	ABA51055	Human breast cell
C 11	72	29.1	219	22	ABA69045	Human foetal liver
C 12	72	29.1	219	22	ABA35989	Probe #14455 for g
C 13	72	29.1	219	22	AAK17358	Human brain expres
C 14	72	29.1	219	22	AAK43155	Human bone marrow
C 15	72	29.1	219	22	AAI23927	Probe #13860 for g
C 16	72	29.1	219	22	AAI49233	Probe #17919 used
C 17	72	29.1	219	22	AAI09526	Probe #9517 used t
C 18	72	29.1	219	24	ABS17231	Human genome-deriv
C 19	66	26.7	198	17	AAI28165	Senescence-related
C 20	41	16.6	362	22	ABA45937	Human breast cell
C 21	41	16.6	362	22	ABA56464	Human foetal liver
C 22	41	16.6	362	22	ABA26097	Probe #4563 for ge
C 23	41	16.6	362	22	AAK04623	Human brain expres
C 24	41	16.6	362	22	AAK30134	Human bone marrow
C 25	41	16.6	362	22	AAI14733	Probe #4666 for ge
C 26	41	16.6	362	22	AAI36098	Probe #4784 used t
C 27	41	16.6	362	22	AAI04536	Probe #4527 used t
C 28	41	16.6	362	24	ABS04715	Human genome-deriv
C 29	40	16.2	420	22	AAH55616	Human breast tumou
C 30	12	4.9	2191	9	AAH80655	Sequence encoding
C 31	9	3.6	436	24	ABN76096	Human RNA polymera
C 32	9	3.6	1360	23	AAAS9785	Propionibacterium
C 33	9	3.6	4188	20	AAAS5767	Drosophila Robo 1
C 34	9	3.6	4188	20	AAAS7250	Drosophila sp. ROB
C 35	9	3.6	4355	23	ABL22881	Drosophila melanog
C 36	9	3.6	8410	23	ABL22880	Drosophila melanog
C 37	9	3.6	11470	23	ABL21296	Drosophila melanog
C 38	9	3.6	53178	23	AAAS9543	Propionibacterium
C 39	9	3.6	96583	21	AAF22297	BAC containing rep
C 40	9	3.2	26	22	AAH22262	Stannocalcin prec
C 41	8	3.2	77	22	AAF73631	HGF nucleic acid 1
C 42	8	3.2	162	22	ABN70013	Streptococcus poly
C 43	8	3.2	324	22	AAAS06373	Streptococcus pyog
C 44	8	3.2	416	23	AAD23428	Human lung tumour
C 45	8	3.2	433	22	ABA08525	Human neuropilin-2
C 46	8	3.2	938	24	ABQ13648	Oligonucleotide fo
C 47	8	3.2	938	24	ABQ13649	Oligonucleotide fo
C 48	8	3.2	1000	22	AAAS0815	Human cDNA encodin
C 49	8	3.2	3006	24	ABQ69272	Listeria innocua D
C 50	8	3.2	3024	24	ABQ67866	Listeria innocua D
C 51	8	3.2	3153	20	AAZ77530	Human secreted pro
C 52	8	3.2	3153	21	AAZ59472	Human secreted pro
C 53	8	3.2	3568	21	AAZ98491	DNA encoding a mai
C 54	8	3.2	3776	22	AAZ58263	Corn cellulose syn
C 55	8	3.2	6707	22	AAAS2417	Human polynucleoti
C 56	8	3.2	6848	22	AAAS2418	Human polynucleoti
C 57	8	3.2	7479	23	ABLI4528	Drosophila melanog
C 58	8	3.2	7525	22	AAAS01192	Fertilisation-inde
C 59	8	3.2	7545	22	ABA09525	Human secreted pro
C 60	8	3.2	7545	22	AAAS3401	Human polynucleoti
C 61	8	3.2	7545	22	AAAS3402	Human polynucleoti
C 62	8	3.2	8911	22	ABA06809	Human genomic DNA
C 63	8	3.2	8911	22	AAAS41748	Genomic sequence #
C 64	8	3.2	10302	24	ABK81961	cDNA encoding huma
C 65	8	3.2	10386	23	AAAS76114	DNA encoding novel
C 66	8	3.2	14286	20	AAAI3099	Enterococcus faeca
C 67	8	3.2	32768	20	AAAI3336	Enterococcus faeca

944	6	2.4	95	21	AAA35567	Microsatellite nuc
945	6	2.4	95	21	AAA35568	Microsatellite nuc
946	6	2.4	95	21	AAA35569	Microsatellite nuc
947	6	2.4	97	24	ABL59281	Nucleotide sequenc
948	6	2.4	97	24	AAD25614	MLL-AP4/98(+) chim
949	6	2.4	98	21	AAA35562	Microsatellite nuc
950	6	2.4	99	21	AAA35563	Human secreted pro
951	6	2.4	100	21	AAX29367	Antimicrobial pept
C 952	6	2.4	102	22	ABA72223	Human foetal liver
C 953	6	2.4	102	22	AAK20645	Human brain expres
C 954	6	2.4	102	22	AAK46789	Human bone marrow
C 955	6	2.4	102	22	AAI52628	Probe #21314 used
C 956	6	2.4	103	21	AAZ29366	Antimicrobial pept
C 957	6	2.4	105	21	AAA35571	Microsatellite nuc
C 958	6	2.4	105	22	ABA48866	Human breast cell
C 959	6	2.4	105	22	AAI21704	Probe #11637 for g
C 960	6	2.4	105	22	AAF75432	Codon-optimised HP
C 961	6	2.4	113	23	ABV00929	Human prostate exp
C 962	6	2.4	114	13	AAQ23247	Nematode resistant
C 963	6	2.4	114	16	AAT21530	Human gene signatu
C 964	6	2.4	116	21	AAC21599	Human secreted pro
C 965	6	2.4	117	20	AAK16062	DNA encoding lytic
C 966	6	2.4	117	20	AAK19278	Extracellular loca
C 967	6	2.4	120	22	ABA74029	Human foetal liver
C 968	6	2.4	120	22	ABA39091	Probe #17557 for g
C 969	6	2.4	120	22	AAK22482	Human brain expres
C 970	6	2.4	120	22	AAK48650	Human bone marrow
C 971	6	2.4	120	22	AAH74363	Nucleotide sequenc
C 972	6	2.4	120	22	AAI26289	Probe #16222 for g
C 973	6	2.4	120	22	AAI54478	Probe #23164 used
C 974	6	2.4	120	22	ABS23296	Human genome-deriv
C 975	6	2.4	123	24	ABN69729	Streptococcus poly
C 976	6	2.4	124	18	AAV79082	Staphylococcus aur
C 977	6	2.4	125	20	AAH86956	Human single nucle
C 978	6	2.4	129	21	AAC29030	Human secreted pro
C 979	6	2.4	131	19	AAK12762	Human biallelic po
C 980	6	2.4	131	20	AAH86528	Human single nucle
C 981	6	2.4	131	22	AAH33505	Human cDNA encodn
C 982	6	2.4	131	22	AAH37743	Novel human diagno
C 983	6	2.4	133	21	AAH58232	D. immitis ankyrin
C 984	6	2.4	133	21	AAH58233	D. immitis ankyrin
C 985	6	2.4	133	22	ABA51094	Human breast cell
C 986	6	2.4	133	22	ABA69088	Human foetal liver
C 987	6	2.4	133	22	ABA36029	Probe #14495 for g
C 988	6	2.4	133	22	AAK17400	Human brain expres
C 989	6	2.4	133	22	AAK43197	Human bone marrow
C 990	6	2.4	133	22	AAI23974	Probe #13907 for g
C 991	6	2.4	133	22	AAI49274	Probe #17960 used
C 992	6	2.4	133	22	AAI09564	Probe #9555 used t
C 993	6	2.4	133	24	ABS17278	Human genome-deriv
C 994	6	2.4	133	24	AAI37918	Dirofilaria immiti
C 995	6	2.4	133	24	AAI37919	Complement strand
C 996	6	2.4	134	15	AAQ77387	Human genome fragm
C 997	6	2.4	136	19	AAV19191	Human XAG growth f
C 998	6	2.4	136	22	ABA51335	Human breast cell
C 999	6	2.4	136	22	ABA69346	Human foetal liver
C1000	6	2.4	136	22	ABA36276	Probe #14742 for g

ALIGNMENTS

RESULT 1
AAA97594
ID AAA97594 standard; cDNA; 741 BP.
XX
XX
AAA97594;
AC
XX
XX
02-FEB-2001 (first entry)
DT
DT
XX
XX
DE Human stanniocalcin cDNA.
XX
XX
KW Human; stanniocalcin; SRC; osteogenesis; bone disease; osteoporosis;
KW mineral metabolism regulator; prophylaxis; therapy; ss.

QY 161 AsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp 180
 Db 481 AACAGACTTGTCCGAAGCCTGCTGGAATGTGATGAAGACACAGTCAGCAATCAGAGAC 540
 QY 181 SerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
 Db 541 AGCCTGATGGAGAAATTTGGGCTTAACATGGCCAGCCCTTCCACATCTCTGAGACAGAC 600
 QY 201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgArgThrAsnGluProGln 220
 Db 601 CACTGTGCCCAACACACCCAGAGTGACTTCAACAGGAGACGCCAATGAGCGCGAG 660
 QY 221 LysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHisIleLys 240
 Db 661 AAGCTGAAAGTCTCTCTCAGGAACCTCCGAGGTGAGGAGTCTCCCTCCACATCAAA 720
 QY 241 ArgThrSerHisGluSerAla 247
 Db 721 CGCACATCCCATGAGAGTGCA 741
 RESULT 2
 AAA11145
 ID AAA11145 standard; cDNA; 741 BP.
 XX
 AC AAA11145;
 XX
 DT 26-SEP-2000 (first entry)
 XX
 DE Human stanniocalcin coding sequence.
 XX
 KW PCR primer; human; stanniocalcin; inhibitor; differentiation; maturation;
 KW adipocyte; obesity; diabetes; heart disease; ss.
 XX
 OS Homo sapiens.
 PN WO200016795-A1.
 XX
 PD 30-MAR-2000.
 XX
 PF 17-SEP-1999; 99WO-JP05080.
 XX
 PR 17-SEP-1999; 98JP-0263004.
 XX
 PA (SNOW) SNOW BRAND MILK PROD CO LTD.
 XX
 PI Goto M, Tomoyasu A, Yamaguchi K, Kinoshita M, Nakagawa N;
 XX
 DR WPI: 2000-283445/24.
 DR P-PSDB; AAY2901.
 XX
 PT Treating or preventing obesity, which is a risk factor for diabetes,
 PT hypertension and heart disease, comprises administering an agent
 PT containing stanniocalcin
 XX
 PS Example 1; Page 14-15; 19pp; Japanese.
 XX
 CC This sequence represents the coding sequence for the human stanniocalcin
 CC protein. The stanniocalcin gene was isolated from IMR-90 cells.
 CC Stanniocalcin is an inhibitor of the differentiation and maturation of
 CC adipocytes. The protein is used for preventing and treating obesity which
 CC is a risk factor for diabetes, hypertension, and heart disease.
 XX
 SQ Sequence 741 BP; 201 A; 209 C; 183 G; 148 T; 0 other;
 Alignment Scores:
 Pred. No.: 2,918-246 Length: 741
 Score: 247.00 Matches: 247
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 21 Gaps: 0
 US-09-705-500A-3 (1-247) x AAA11145 (1-741)

QY 1 MetLeuGlnAsnSerAlaValLeuLeuValLeuValIleSerAlaSerAlaThrHisGlu 20
 Db 1 ATGCTCCAAAACTCAGCAGTCTCTTGGTGTGGTGATCAGTGTCTCTGCAACCCATCAG 60
 QY 21 AlaGluGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
 Db 61 GCGAGAGCAAGATGACTCTGTGAGCCCCAGGAAATCCCCAGTGGCGGCCCAAACTCAGCT 120
 QY 41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyValAlaPheAlaCysLeu 60
 Db 121 GAAGTGGTTCGCTGCCTCAACAGTCTCTACAGTGGCTGCGGGGCTTTTGCATGCCCTG 180
 QY 61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
 Db 181 GAAAACTCCACTGTGACACAGATGGGATGTATGACATCTGTAAATCTCTTCTGTAGACG 240
 QY 81 AlaAlaLysPheAspThrGlnGlyAlaPheValLysGluSerLeuLysCysIleAla 100
 Db 241 GCTGCTAAATTTGACACTCAGGGAAGAGCATTCGTCAAAGAGAGCTTAAATGTCATGCC 300
 QY 101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
 Db 301 AACGGGTGTCACCTCAAGTCTCTCTGCCATTCGAGGTGCTCCACTTCCAAAGGATG 360
 QY 121 IleAlaGluValGlnGluGlyCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
 Db 361 ATTGCTGAGGTGCAGGAAGAGTGTACAGCAAGCTGAAATGTGTGAGCATGCCAAGCGG 420
 QY 141 AsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
 Db 421 AACCTGAAGCCATCCTCAGGTGCTCCAGTGCCTCCCAATCACTTCTCCACAGATACTAT 480
 QY 161 AsnArgLeuValArgSerLeuGluCysAspGluAspThrValSerThrIleArgAsp 180
 Db 481 AACAGACTTGTCCGAAGCCTGCTGGAATGTGATGAGACACAGTCAGCAATCAGAGAC 540
 QY 181 SerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
 Db 541 AGCCTGATGGAGAAATTTGGGCTTAACATGGCCAGCTCTTCCACATCTCTGAGACAGAC 600
 QY 201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgArgThrAsnGluProGln 220
 Db 601 CACTGTGCCCAACACACCCAGAGTGACTTCAACAGGAGACGCCAATGAGCGCGAG 660
 QY 221 LysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHisIleLys 240
 Db 661 AAGCTGAAAGTCTCTCTCAGGAACCTCCGAGGTGAGGAGTCTCTCCCTCCACATCAAA 720
 QY 241 ArgThrSerHisGluSerAla 247
 Db 721 CGCACATCCCATGAGAGTGCA 741
 RESULT 3
 ABL40225
 ID ABL40225 standard; cDNA; 744 BP.
 XX
 AC ABL40225;
 XX
 DT 23-MAY-2002 (first entry)
 XX
 DE Human stanniocalcin 1 encoding cDNA.
 XX
 KW Human; stanniocalcin 1; osteopathic; osteogenesis failure; osteoporosis;
 KW bone mass reduction; traumatic bone injury; osteomalacia; bone disease;
 KW rheumatic bone disease; cancer associated bone disease; rickets;
 OS arthritic deformans; gene; ss.
 XX
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT 1..744
 FT CDS /*tag= a

PT useful for the prevention, diagnosis and treatment of breast cancer -
 PS Claim 24; Page 168; 22lpp; English.
 XX
 CC The present sequence is a human breast tumour protein coding sequence.
 CC This sequence may be used in the prevention, diagnosis and treatment of
 CC diseases associated with inappropriate expression of the breast tumour
 CC protein e.g. breast cancer. For example, this sequence may be used to
 CC treat disorders associated with decreased expression by rectifying
 CC mutations or deletions in a patient's genome that affect the activity of
 CC breast tumour protein by expressing inactive proteins or to supplement
 CC the patient's own production of the breast tumour protein. Additionally,
 CC the present sequence may be used to produce the breast tumour protein, by
 CC inserting the nucleic acids into a host cell and culturing the cell to
 CC express the protein. The present sequence and its complementary sequences
 CC may also be used as DNA probes in diagnostic assays to detect and
 CC quantitate the presence of similar nucleic acids in samples, and
 CC therefore which patients may be in need of restorative therapy.
 XX
 SQ Sequence 585 BP; 171 A; 163 C; 136 G; 110 T; 5 other;

Alignment Scores:
 Pred. No.: 3.2e-156 Length: 585
 Score: 160.00 Matches: 160
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 64.78% Indels: 0
 DB: 22 Gaps: 0

US-09-705-500A-3 (1-247) x AAH55624 (1-585)

QY 88 GlyLysAlaPheValLysGluSerLeuLysCysIleAlaAsnGlyValThrSerLysVal 107
 Db 33 GGAAGAGCATTCCTCAAGAGAGCTTAAATGCATCGCCAGGGGTACCTCCCAAGGTC 92
 QY 108 PheLeuAlaIleArgArgCysSerThrPheGlnArgMetIleAlaGluValGlnGlu 127
 Db 93 TTCCTCGCCATTCGGAGGTCCTCACTTTCCAAAGGATGATTGCTGAGGTGAGGAAG 152
 QY 128 CysTyrSerLysLeuAsnValCysSerIleAlaLysArgAsnProGluAlaIleThrGlu 147
 Db 153 TGCTACAGCAAGCTGATGTGTGCAGCATCGCCAGCGGAACCTGAGCCATCTCTGAG 212
 QY 148 ValValGlnLeuProAsnHisPheSerAsnArgTyrTyrAsnArgLeuValArgSerLeu 167
 Db 213 GTGCTCCAGCTGCCAATCACTTCTCCACAGATATAACAGACTTGTCCGAAGCCTG 272
 QY 168 LeuGluCysAspGluAspThrValSerThrIleArgAspSerLeuMetGluLysIleGly 187
 Db 273 CTGGAATGTGATGAAGACACACGTACGACCAATCAGAGACAGCCTGATGGAGAAATGGG 332
 QY 188 ProAsnMetAlaSerLeuPheHisIleLeuGlnThrAspHisCysAlaGlnThrHisPro 207
 Db 333 CCTACATGCGCAGCTCTTCCACATCTCTGAGACAGACCATCTGTGCCCAACACACCA 392
 QY 208 ArgAlaAspPheAsnArgArgThrAsnGluProGlnLysLeuLysValLeuLeuArg 227
 Db 393 CGAGCTGACTTCAACAGGAGAGCGCACCATGAGCGCAGAACTGAAAGTCTCTCTCAGG 452
 QY 228 AsnLeuArgGlyGluGluAspSerProSerHisIleLysArgThrSerHisGluSerAla 247
 Db 453 AACCTCCGAGGTGAGGAGGACTCTCCCTCCACATCAACAGCACATCCCATGAGAGTGCA 512

RESULT 10
 ID ABA51055/c
 XX ABA51055 standard; DNA; 219 BP.
 AC ABA51055;
 XX
 DT 01-FEB-2002 (first entry)
 XX Human breast cell single exon nucleic acid probe #9750.
 XX

KW Human; microarray; single exon probe; gene expression; breast;
 KW disease; cancer; ss.
 XX
 OS Homo sapiens.
 PN WO200157271-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 30-JAN-2001; 2001WO-US00662.
 XX
 PR 04-FEB-2000; 2000US-0180312.
 PR 26-MAY-2000; 2000US-0207456.
 PR 30-JUN-2000; 2000US-0608408.
 PR 03-AUG-2000; 2000US-0632366.
 PR 21-SEP-2000; 2000US-0234687.
 PR 27-SEP-2000; 2000US-0236359.
 PR 04-OCT-2000; 2000GB-0024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX
 DR WPI; 2001-496933/54.
 XX
 PT New spatially-addressable set of single exon nucleic acid probes,
 PT useful for measuring gene expression in sample derived from human
 PT breast, comprises number of single exon nucleic acid probes -
 XX
 PS Claim 4; SEQ ID NO 9750; 327pp + sequence listing; English.
 XX
 CC The invention relates to a spatially-addressable set of single exon
 CC nucleic acid probes for measuring gene expression in a sample derived
 CC from human breast and BT 474 cells. The method involves contacting
 CC the probes with a collection of detectably labelled nucleic acids
 CC derived from mRNA of human breast, and then measuring the label
 CC bound to each probe of the microarray. The probes are useful for
 CC verifying the expression of regions of genomic DNA predicted to
 CC encode proteins. They are useful for gene discovery, and for
 CC determining predisposition and/or prognosing breast disease. Gene
 CC expression analysis is useful for assessing the toxicity of chemical
 CC agents on cells. The microarray of this invention presents a far greater
 CC diversity of probes for measuring gene expression, with far less bias
 CC than expressed sequence tag microarrays. The method is suitable for
 CC rapid production of functional information from genomic sequence. The
 CC present sequence is a single exon nucleic acid probe of the invention.
 CC Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 219 BP; 43 A; 55 C; 60 G; 61 T; 0 other;

Alignment Scores:
 Pred. No.: 1.86e-65 Length: 219
 Score: 72.00 Matches: 72
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 29.15% Indels: 0
 DB: 22 Gaps: 0

US-09-705-500A-3 (1-247) x ABA51055 (1-219)

QY 88 GlyLysAlaPheValLysGluSerLeuLysCysIleAlaAsnGlyValThrSerLysVal 107
 Db 219 GGAAGAGCATTCCTCAAGAGAGCTTAAATGCATCGCCAGGGGTACCTCCCAAGGTC 160
 QY 108 PheLeuAlaIleArgArgCysSerThrPheGlnArgMetIleAlaGluValGlnGlu 127
 Db 159 TTCCTCGCCATTCGGAGGTCCTCACTTTCCAAAGGATGATTGCTGAGGTGAGGAAG 100
 QY 128 CysTyrSerLysLeuAsnValCysSerIleAlaLysArgAsnProGluAlaIleThrGlu 147
 Db 99 TGCTACAGCAAGCTGAATGTGTGAGCATCGCCAGCGGAACCTTCAAGCCATCTCTGAG 40

QY 148 ValValGlnLeuProAsnHisPheSerAsnArgTyr 159
 DB 39 GTCTCCAGCTGCCCAATCACTTCTCCACAGGTAC 4

RESULT 11

ABA69045/c
 ID ABA69045 standard; DNA; 219 BP.

XX ABA69045;

DT 01-FEB-2002 (first entry)

DE Human foetal liver single exon nucleic acid probe #17350.

XX Human; foetal liver; gene expression; single exon nucleic acid probe; ss.

OS Homo sapiens.

PN WO200157277-A2.

XX 09-AUG-2001.

PF 30-JAN-2001; 2001WO-US00669.

XX 04-FEB-2000; 2000US-0180312.

PR 26-MAY-2000; 2000US-0207456.

PR 30-JUN-2000; 2000US-0608408.

PR 03-AUG-2000; 2000US-0632366.

PR 21-SEP-2000; 2000US-0234687.

PR 27-SEP-2000; 2000US-0236359.

PR 04-OCT-2000; 2000GB-0024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-483447/52.

XX Human genome-derived single exon nucleic acid probes useful for

PT analyzing gene expression in human fetal liver -

XX Claim 4; SEQ ID NO 17350; 639pp + sequence listing; English.

XX The invention relates to a single exon nucleic acid probe for

CC measuring human gene expression in a sample derived from human foetal

CC liver. The single exon nucleic acid probes may be used for predicting,

CC measuring and displaying gene expression in samples derived from human

CC fetal liver. The present sequence is a single exon nucleic acid

CC probe of the invention.

CC Note: The sequence data for this patent did not form part of the

CC printed specification, but was obtained in electronic format directly

CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 219 BP; 43 A; 55 C; 60 G; 61 T; 0 other;

Alignment Scores:

Pred. No.: 1.86e-65 Length: 219

Score: 72.00 Matches: 72

Percent Similarity: 100.00% Conservativity: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 29.15% Indels: 0

DB: 22 Gaps: 0

QY 128 CystTyrSerLysLeuAsnValCysSerIleAlaLysArgAsnProGluAlaIleThrGlu 147
 DB 99 TGTACACGCAAGCTGCAATGTGTGCAGCATCGCCAGCGGAACCTGAAGCCATCACTGAG 40

QY 148 ValValGlnLeuProAsnHisPheSerAsnArgTyr 159

DB 39 GTCTCCAGCTGCCCAATCACTTCTCCACAGGTAC 4

RESULT 12

ABA35989/c

ID ABA35989 standard; DNA; 219 BP.

XX ABA35989;

DT 23-JAN-2002 (first entry)

DE Probe #14455 for gene expression analysis in human heart cell sample.

XX Human; gene expression; heart; microarray; vascular system; probe;

KW cardiovascular disease; hypertension; cardiac arrhythmia;

KW congenital heart disease; ss.

XX Homo sapiens.

XX WO200157274-A2.

PD 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US00666.

XX 04-FEB-2000; 2000US-0180312.

PR 26-MAY-2000; 2000US-0207456.

PR 30-JUN-2000; 2000US-0608408.

PR 03-AUG-2000; 2000US-0632366.

PR 21-SEP-2000; 2000US-0234687.

PR 27-SEP-2000; 2000US-0236359.

PR 04-OCT-2000; 2000GB-0024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488899/53.

XX Single exon nucleic acid probes for analyzing gene expression in human

PT hearts -

XX Claim 4; SEQ ID No 14455; 530pp; English.

XX The present invention relates to single exon nucleic acid probes for

CC measuring human gene expression in a sample derived from human heart. The

CC present sequence is one such probe. The probes may be used for

CC predicting, measuring and displaying gene expression in samples derived

CC from the human heart via microarrays. By measuring gene expression, the

CC probes are useful for predicting, diagnosing, grading, staging,

CC monitoring and prognosing diseases of the human heart and vascular system

CC e.g. cardiovascular disease, hypertension, cardiac arrhythmias and

CC congenital heart disease.

CC Note: The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from WIPO

CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 219 BP; 43 A; 55 C; 60 G; 61 T; 0 other;

Alignment Scores:

Pred. No.: 1.86e-65 Length: 219

Score: 72.00 Matches: 72

Percent Similarity: 100.00% Conservativity: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 29.15% Indels: 0

DB: 22 Gaps: 0

QY 88 GlyLysAlaPheValLysGluSerLeuLysCysIleAlaAsnGlyValThrSerLysVal 107

DB 219 GGAAGAAGCATTCGTCAAGAGAGCTAATAATGCATCGCCAGCGGTCACTCCAAAGGTC 160

QY 108 PheLeuAlaIleArgCysSerThrPheGlnArgMetIleAlaGluValGlnGlu 127

DB 159 TTCTTCGCCAATTCGGAGGTGCTCCACTTTCCAAAGGATGATTGCTGAGGTGAGGAAG 100

US-09-705-500A-3 (1-247) x ABA35989 (1-219)

QY 88 GlyLysAlaPheValLysGluSerLeuLysCysIleAlaAsnGlyValThrSerLysVal 107
DB 219 GGAAGAAGCATTCGTCAAGAGAGCTTAAATGCTATGCTCAACGGGTCACTCCAAAGGTC 160
QY 108 PheLeuAlaIleArgArgCysSerThrPheGlnArgMetIleAlaGluValGlnGlu 127
DB 159 TTCCTCGCCATTCGGAGGTCCTCACTTCCAAAGGATGATTCGTAGGTGAGGAAGAG 100
QY 128 CysTyrSerLysLeuAsnValCysSerIleAlaLysArgAsnProGluAlaIleThrGlu 147
DB 99 TGTACAGCAAGCTGAATGTGTGCAGCATCGCAAGCGGACCTTGAAGCCATCACTGAG 40
QY 148 ValValGlnLeuProAsnHisPheSerAsnArgTyr 159
DB 39 GTCGTCCAGCTGCCCAATCACTTCTCCACAGGTAC 4

RESULT 13

AAK17358/c
ID AAK17358 standard; DNA; 219 BP.
XX AAK17358;
DT 05-NOV-2001 (first entry)
DE Human brain expressed single exon probe SEQ ID NO: 17349.
KW Human; brain expressed exon; gene expression analysis; probe;
KW microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
KW epilepsy; cancer; ss.
XX Homo sapiens.
OS
XX
XX WO200157275-A2.
PN
XX
XX 09-AUG-2001.
PD
XX
XX 30-JAN-2001; 2001WO-US00667.
PF
XX
XX 04-FEB-2000; 2000US-0180312.
PR
XX 26-MAY-2000; 2000US-0207456.
PR
XX 30-JUN-2000; 2000US-0608408.
PR
XX 03-AUG-2000; 2000US-0632366.
PR
XX 21-SEP-2000; 2000US-0234687.
PR
XX 27-SEP-2000; 2000US-0236359.
PR
XX 04-OCT-2000; 2000GB-0024263.
PA (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-483446/52.
XX Single exon nucleic acid probes for analyzing gene expression in human
PT brains -
XX
XX Example 4; SEQ ID NO: 17349; 650pp + Sequence Listing; English.
PS
XX The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC brain. They can be used to measure gene expression in brain cell samples,
CC which may enable the diagnosis and improved treatment of nervous system
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC epilepsy and cancers. The present sequence is one of the probes of the
CC invention.
XX
SQ Sequence 219 BP; 43 A; 55 C; 60 G; 61 T; 0 other;

Alignment Scores:
Pred. No.: 1,86e-65 Length: 219
Score: 72.00 Matches: 72
Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 29.15% Indels: 0
DB: 22 Gaps: 0

US-09-705-500A-3 (1-247) x AAK17358 (1-219)

QY 88 GlyLysAlaPheValLysGluSerLeuLysCysIleAlaAsnGlyValThrSerLysVal 107
DB 219 GGAAGAAGCATTCGTCAAGAGAGCTTAAATGCTATGCTCAACGGGTCACTCCAAAGGTC 160
QY 108 PheLeuAlaIleArgArgCysSerThrPheGlnArgMetIleAlaGluValGlnGlu 127
DB 159 TTCCTCGCCATTCGGAGGTCCTCACTTCCAAAGGATGATTCGTAGGTGAGGAAGAG 100
QY 128 CysTyrSerLysLeuAsnValCysSerIleAlaLysArgAsnProGluAlaIleThrGlu 147
DB 99 TGTACAGCAAGCTGAATGTGTGCAGCATCGCAAGCGGACCTTGAAGCCATCACTGAG 40
QY 148 ValValGlnLeuProAsnHisPheSerAsnArgTyr 159
DB 39 GTCGTCCAGCTGCCCAATCACTTCTCCACAGGTAC 4

RESULT 14

AAK43155/c
ID AAK43155 standard; DNA; 219 BP.
XX AAK43155;
DT 06-NOV-2001 (first entry)
DE Human bone marrow expressed single exon probe SEQ ID NO: 17712.
KW Human; bone marrow expressed exon; gene expression analysis; probe;
KW microarray; cancer; leukaemia; lymphoma; myeloma; ss.
XX Homo sapiens.
OS
XX
XX WO200157276-A2.
PN
XX
XX 09-AUG-2001.
PD
XX
XX 30-JAN-2001; 2001WO-US00668.
PF
XX
XX 04-FEB-2000; 2000US-0180312.
PR
XX 26-MAY-2000; 2000US-0207456.
PR
XX 30-JUN-2000; 2000US-0608408.
PR
XX 03-AUG-2000; 2000US-0632366.
PR
XX 21-SEP-2000; 2000US-0234687.
PR
XX 27-SEP-2000; 2000US-0236359.
PR
XX 04-OCT-2000; 2000GB-0024263.
PA (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488900/53.
XX

XX Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human bone marrow -
XX
XX Example 4; SEQ ID NO: 17712; 658pp + Sequence Listing; English.

PS The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC bone marrow. They can be used to measure gene expression in bone marrow
CC samples, which may enable the improved diagnosis and treatment of cancers
CC such as lymphoma, leukaemia and myeloma. The present sequence is one of
CC the probes of the invention.
XX
SQ Sequence 219 BP; 43 A; 55 C; 60 G; 61 T; 0 other;

Alignment Scores:
Pred. No.: 1,86e-65 Length: 219

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 12, 2003, 22:03:00 ; Search time 67 Seconds
(without alignments)
1130.584 Million cell updates/sec

Title: US-09-705-500A-3

Perfect score: 247

Sequence: 1 MLQNSAVLLVLVISASATHE.....NLRGEEDPSHIKRTSHESA 247

Scoring table:

OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 441362 seqs, 153338381 residues

Word size: 1

Total number of hits satisfying chosen parameters: 878589

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlp
-O=/cgn2_1/USPTO spoil/US09705500/runat 06062003 113645 8001/app query fasta_1.391
-DB=Issued Patents NA -QFMT=fastap -SUFFIX=oligo.rn1 -MINMATCH=0.1 -LOOFCU=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=numan40.cdi
-LIST=1000 -DOCALIGN=200 -THR SCORE=quality -THR MIN=1 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09705500 @CEN 1 1 36 @runat 06062003 113645 8001 -NCPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :

Issued Patents NA:
1: /cgn2_6/ptodata/2/ina/5A COMB.seq:
2: /cgn2_6/ptodata/2/ina/5B COMB.seq:
3: /cgn2_6/ptodata/2/ina/6A COMB.seq:
4: /cgn2_6/ptodata/2/ina/6B COMB.seq:
5: /cgn2_6/ptodata/2/ina/PTCUS COMB.seq:
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	247	100.0	771	2	US-08-208-005C-1
2	247	100.0	771	2	US-09-038-597A-1
3	247	100.0	771	2	US-08-431-117A-1
4	8	3.2	77	4	US-09-364-539-181
5	8	3.2	3153	4	US-09-175-928-9
6	8	3.2	44377	2	US-08-804-227C-7
7	8	3.2	44377	2	US-08-804-198-1
8	7	2.8	27	1	US-08-325-553-30
9	7	2.8	27	2	US-08-208-005C-3
10	7	2.8	27	2	US-09-038-597A-3
11	7	2.8	27	2	US-08-394-152A-30
12	7	2.8	27	2	US-08-431-117A-3

962 2.4 2667 2 US-08-469-412A-1 Sequence 1, Appli
963 2.4 2667 4 US-09-021-715-1 Sequence 1, Appli
964 2.4 2667 4 US-08-511-485-5 Sequence 5, Appli
965 2.4 2681 2 US-08-732-192A-1 Sequence 1, Appli
966 2.4 2694 1 US-08-465-998A-1 Sequence 1, Appli
967 2.4 2694 1 US-08-465-998A-3 Sequence 3, Appli
968 2.4 2694 2 US-08-465-994C-1 Sequence 1, Appli
969 2.4 2694 2 US-08-465-994C-3 Sequence 3, Appli
970 2.4 2694 2 US-08-966-145-1 Sequence 1, Appli
971 2.4 2694 2 US-08-966-145-3 Sequence 3, Appli
972 2.4 2704 4 US-09-221-017B-94 Sequence 94, Appli
973 2.4 2706 4 US-09-134-001C-2552 Sequence 2552, Ap
974 2.4 2724 2 US-08-658-665-37 Sequence 37, Appli
975 2.4 2724 4 US-08-796-101-1 Sequence 1, Appli
976 2.4 2724 4 US-09-085-273-37 Sequence 37, Appli
977 2.4 2728 4 US-09-025-769B-299 Sequence 299, Appli
978 2.4 2737 4 US-09-484-970B-29 Sequence 29, Appli
979 2.4 2742 3 US-08-911-853-16 Sequence 16, Appli
980 2.4 2742 4 US-09-479-409-16 Sequence 16, Appli
981 2.4 2742 4 US-09-479-453-16 Sequence 16, Appli
982 2.4 2754 2 US-09-028-361A-1 Sequence 1, Appli
983 2.4 2755 3 US-08-749-522-2 Sequence 2, Appli
984 2.4 2757 1 US-08-306-691B-48 Sequence 48, Appli
985 2.4 2757 5 PCT-US93-06251-79 Sequence 79, Appli
986 2.4 2760 1 US-08-101-593-1 Sequence 1, Appli
987 2.4 2760 1 US-08-101-593-3 Sequence 3, Appli
988 2.4 2763 4 US-09-030-335-3 Sequence 3, Appli
989 2.4 2781 4 US-09-302-812-7 Sequence 7, Appli
990 2.4 2781 4 US-09-511-477-7 Sequence 7, Appli
991 2.4 2781 4 US-09-511-507-7 Sequence 7, Appli
992 2.4 2784 1 US-08-104-073-3 Sequence 3, Appli
993 2.4 2784 1 US-08-104-073-3 Sequence 3, Appli
994 2.4 2784 1 US-08-351-413-10 Sequence 10, Appli
995 2.4 2784 1 US-08-351-413-10 Sequence 10, Appli
996 2.4 2784 2 US-09-025-583-10 Sequence 10, Appli
997 2.4 2784 2 US-09-025-583-10 Sequence 10, Appli
998 2.4 2793 1 US-07-646-537B-1 Sequence 1, Appli
999 2.4 2798 4 US-09-318-448-34 Sequence 34, Appli
c1000 2.4 2799 4 US-08-887-534A-44 Sequence 44, Appli

ALIGNMENTS

RESULT 1
US-08-208-005C-1
; Sequence 1, Application US/08208005C
; Patent No. 5837498
; GENERAL INFORMATION:
; APPLICANT: OLSEN, ET AL.
; TITLE OF INVENTION: Corpuscles of Stannius Protein, Stanniocalcin
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/208,005C
; FILING DATE: 8 MARCH 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: FERRARO, GREGORY D.

REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-78
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 771 BASE PAIRS
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
MOLECULE TYPE: CDNA
US-08-208-005C-1
Alignment Scores:
Pred. No.: 1,24e-249 Length: 771
Score: 247.00 Matches: 247
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
US-09-705-500A-3 (1-247) x US-08-208-005C-1 (1-771)
Qy 1 MetLeuGlnAsnSerAlaValLeuValLeuValIleSerAlaSerAlaThrHisGlu 20
Db 16 ATGCTCCAAAACCTCAGCAGTGTCTTCTGGTGTGTGTGATCAGTCTTCTGCAACCCATGAG 75
Qy 21 AlaGluGlnAsnAppSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
Db 76 GCGGAGCAGAAATGACTCTGTGAGCCCCAGAAATCCCGAGTGGCGGCCCAAAATCAGCT 135
Qy 41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
Db 136 GAAGTGGTTCGTGCTCAACAGTGTCTTACAGTCTGCTGCGGGGCTTTTGATGCTGCTG 195
Qy 61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
Db 196 GAAAACTCCACTGTGTGACACAGATGGGATGTATGACATCTGTAAATCTCTTCTGTACAGC 255
Qy 81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAla 100
Db 256 GCTGCTAAATTTGACACTCAGGGAAGAAAGCATTTGTCAGAGAGAGCTTAAATGCAATCGCC 315
Qy 101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
Db 316 AACGGGTCACTCAAGGTCTTCTCGCCATTCGGAGGTGCTCCACTTCCAAAGGATG 375
Qy 121 IleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
Db 376 ATTGCTGAGGTGCAGGAAGAGTGTACAGCAAGCTGAATGTGTGAGCATGCCAAGCGG 435
Qy 141 AsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
Db 436 AACCTGAAAGCCATCCTGAGGTGCTGAGGTGCTGAGGTGCTGAGGTGCTGAGGTGCTGAG 495
Qy 161 AsnArgLeuValArgSerLeuGluCysAspGluAspThrValSerThrIleArgAsp 180
Db 496 AACAGACTTGTCCGAGGCTGCTGGAATGTGATGAGACAGATCAGCACAATCAGAGAC 555
Qy 181 SerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
Db 556 AGCCTGATGGAGAAATTTGGGCTTAACATGGCCAGCTCTTCCACATCTCTCCAGACAGAC 615
Qy 201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgArgThrAsnGluProGln 220
Db 616 CACTGTGCCCAACACACCCAGAGTCACTTCAACAGAGAGACGACCAATGAGCGGAG 675
Qy 221 LysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHisIleLys 240
Db 676 AAGCTGAAAGTCTCTCTCAGGAACCTCCGAGGTGAGGAGGACTCTCTCCCTCCACATCAA 735
Qy 241 ArgThrSerHisGluSerAla 247

US-09-705-500A-3 (1-247) x US-09-175-928-9 (1-3153)

QY 219 ProGinLysLeuLysValleuLeu 226

Db 2448 CCCAGAGCTGAAAGTCTCTTG 2471

RESULT 6

US-08-804-227C-7

; Sequence 7, Application US/08804227C

; Patent No. 5876991

; GENERAL INFORMATION:

; APPLICANT: DeHoff, Bradley S.

; APPLICANT: Kuhstoss, Stuart A.

; APPLICANT: Rostock, Paul R., Jr.

; APPLICANT: Sutton, Kimberly L.

; TITLE OF INVENTION: POLYKETIDE SYNTHASE GENES

; NUMBER OF SEQUENCES: 15

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: THOMAS G. PLANT 1501

; STREET: LILLY CORPORATE CENTER

; CITY: INDIANAPOLIS

; STATE: IN

; COUNTRY: USA

; ZIP: 46285

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: MS-DOS

; SOFTWARE: ASCII(DOS) Text only

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/804,227C

; FILING DATE: February 21, 1997

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Plant, Thomas G.

; REGISTRATION NUMBER: 35,784

; REFERENCE/DOCKET NUMBER: X-8231

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 317-276-2459

; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 44377 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 350..14002

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 14046..20036

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 20110..31284

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 31329..36071

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 36155..41830

US-08-804-227C-7

Alignment Scores:

Pred. No.: 1.44e+03 Length: 44377

Score: 8.00 Matches: 8

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 3.24% Indels: 0

DB: 2 Gaps: 0

US-09-705-500A-3 (1-247) x US-08-804-227C-7 (1-44377)

QY 162 ArgLeuValArgSerLeuLeuGlu 169

Db 23686 CGACTGGTCCGTCCTCTCGAG 23709

RESULT 7

US-08-804-198-1

; Sequence 1, Application US/08804198

; Patent No. 5945320

; GENERAL INFORMATION:

; APPLICANT: Burgett, Stanley G.

; APPLICANT: Kuhstoss, Stuart A.

; APPLICANT: Rao, Nagardja R.

; APPLICANT: Richardson, Mark A.

; APPLICANT: Rostock, Paul R., Jr.

; TITLE OF INVENTION: PLATENOLIDE SYNTHASE GENE

; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: PAUL R. CANTRELL 1138

; STREET: LILLY CORPORATE CENTER

; CITY: INDIANAPOLIS

; STATE: IN

; COUNTRY: USA

; ZIP: 46285

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: Macintosh

; OPERATING SYSTEM: Macintosh 7.0

; SOFTWARE: Microsoft Word 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/804,198

; FILING DATE:

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: CANTRELL, PAUL R.

; REGISTRATION NUMBER: 36,470

; REFERENCE/DOCKET NUMBER: P9113

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 317-276-3885

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 44377 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 350..14002

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 14046..20036

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 20110..31284

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 31329..36071

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 36155..41830

US-08-804-198-1

Alignment Scores:

Pred. No.: 1.44e+03 Length: 44377

Score: 8.00 Matches: 8

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 3.24% Indels: 0

DB: 2 Gaps: 0

US-09-705-500A-3 (1-247) x US-08-804-198-1 (1-44377)

QY 162 ArgLeuValArgSerLeuLeuGlu 169
Db 23686 CGACTGGTCCGCTCCCTCCGAG 23709

RESULT 8

US-08-325-553-30/c
; Sequence 30, Application US/08325553
; Patent No. 5538866
; GENERAL INFORMATION:
; APPLICANT: Israeli, Ron S.
; APPLICANT: Heston, Warren D.W.
; APPLICANT: Fair, William R.
; TITLE OF INVENTION: THE PROSTATE-SPECIFIC MEMBRANE ANTIGEN
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/325,553
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/973,337A
; FILING DATE: 05 NOV 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 1747/41426
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 664-0525
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo Sapien
; TISSUE TYPE: Carcinoma
; IMMEDIATE SOURCE:
; CLONE: Prostate Specific Membrane Antigen
US-08-325-553-30

Alignment Scores:
Pred. No.: 10.2 Length: 27
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.83% Indels: 0
DB: 1 Gaps: 0

US-09-705-500A-3 (1-247) x US-08-325-553-30 (1-27)

QY 221 LysLeuLysValLeuLeuArg 227
Db 21 AGCTGAAGATTTCCTCGT 1

RESULT 9

US-08-208-005C-3

; Sequence 3, Application US/08208005C
; Patent No. 5837498
; GENERAL INFORMATION:
; APPLICANT: OLSEN, ET AL.
; TITLE OF INVENTION: Corpuscles of Stannius Protein, Stanniocalcin
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/208,005C
; FILING DATE: 8 MARCH 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: FERRARO, GREGORY D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-78
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 BASE PAIRS
; TYPE: NUCLEIC ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; MOLECULE TYPE: Oligonucleotide
US-08-208-005C-3

Alignment Scores:
Pred. No.: 10.2 Length: 27
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.83% Indels: 0
DB: 2 Gaps: 0

US-09-705-500A-3 (1-247) x US-08-208-005C-3 (1-27)

QY 1 MetLeuGlnAsnSerAlaVal 7
Db 7 ATGCTCAAAACTCAGCAGTG 27

RESULT 10

US-09-038-597A-3
; Sequence 3, Application US/09038597A
; Patent No. 5877290
; GENERAL INFORMATION:
; APPLICANT: OLSEN, ET AL.
; TITLE OF INVENTION: Corpuscles of Stannius Protein,
; TITLE OF INVENTION: Stanniocalcin
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/038,597A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/208,005
FILING DATE: 8-MARCH-1994
ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-78
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 BASE PAIRS
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
MOLECULE TYPE: Oligonucleotide
US-09-038-597A-3

Alignment Scores:
Pred. No.: 10.2 Length: 27
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.83% Indels: 0
DB: 2 Gaps: 0

US-09-705-500A-3 (1-247) x US-09-038-597A-3 (1-27)
QY 1 MetLeuGlnAsnSerAlaVal 7
DB 7 ATGCTCCAAACTCAGCAGTG 27

RESULT 11
US-08-394-152A-30/c
Sequence 30, Application US/08394152A
Patent No. 5935818
GENERAL INFORMATION:
APPLICANT: Israeli, Ron S.
APPLICANT: Heston, Warren D.W.
TITLE OF INVENTION: PROSTATE-SPECIFIC MEMBRANE ANTIGEN AND
TITLE OF INVENTION: US\$ THEREOF
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM 330 466 DX2
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/394,152A
FILING DATE: 24-FEB-95
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41426-B

TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo Sapien
TISSUE TYPE: Carcinoma
IMMEDIATE SOURCE:
CLONE: Prostate Specific Membrane Antigen
US-08-394-152A-30

Alignment Scores:
Pred. No.: 10.2 Length: 27
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.83% Indels: 0
DB: 2 Gaps: 0

US-09-705-500A-3 (1-247) x US-08-394-152A-30 (1-27)
QY 221 LysLeuLysValLeuLeuArg 227
DB 21 AAGCTGAAAGTTTTCCTCGT 1

RESULT 12
US-08-431-117A-3
Sequence 3, Application US/08431117A
Patent No. 5994301
GENERAL INFORMATION:
APPLICANT: OLSEN, ET AL.
TITLE OF INVENTION: Corpuscles of Stannius Protein, Stanniocalcin
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/431,117A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/208,005
FILING DATE: 8 MARCH 1994
ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-296
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 BASE PAIRS
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE

TOPOLOGY: LINEAR
MOLECULE TYPE: Oligonucleotide
US-08-431-117A-3

Alignment Scores: 10.2 Length: 27
Pred. No.: 7.00 Matches: 7
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 2.83%
DB: 2 Gaps: 0

US-09-705-500A-3 (1-247) x US-08-431-117A-3 (1-27)

QY 1 MetLeuGlnAsnSerAlaVal 7
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DB 7 ATGCTCCAAACTCAGCAGTG 27

RESULT 13

US-08-208-005C-4/c
; Sequence 4, Application US/08208005C
; Patent No. 5837498
; GENERAL INFORMATION:
; APPLICANT: OLSEN, ET AL.
; TITLE OF INVENTION: Corpuscles of Stannius Protein, Stanniocalcin
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2

OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
FILING DATE: 8 MARCH 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:

FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-78
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 BASE PAIRS
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
MOLECULE TYPE: Oligonucleotide
US-08-208-005C-4

Alignment Scores: 11.7 Length: 31
Pred. No.: 7.00 Matches: 7
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 2.83%
DB: 2 Gaps: 0

US-09-705-500A-3 (1-247) x US-08-208-005C-4 (1-31)

QY 241 ArgThrSerHisGluSerAla 247

DB 31 CGCACATCCCATGAGAGTGCA 11
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RESULT 14

US-09-038-597A-4/c
; Sequence 4, Application US/09038597A
; Patent No. 5877290
; GENERAL INFORMATION:
; APPLICANT: OLSEN, ET AL.
; TITLE OF INVENTION: Corpuscles of Stannius Protein,
; TITLE OF INVENTION: Stanniocalcin
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/038,597A
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/208,005
FILING DATE: 8-MARCH-1994

ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-78
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 BASE PAIRS
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
MOLECULE TYPE: Oligonucleotide
US-09-038-597A-4

Alignment Scores: 11.7 Length: 31
Pred. No.: 7.00 Matches: 7
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 2.83%
DB: 2 Gaps: 0

US-09-705-500A-3 (1-247) x US-09-038-597A-4 (1-31)
QY 241 ArgThrSerHisGluSerAla 247
|||||

DB 31 CGCACATCCCATGAGAGTGCA 11
|||||

RESULT 15

US-08-431-117A-4/c
; Sequence 4, Application US/08431117A
; Patent No. 5994301
; GENERAL INFORMATION:
; APPLICANT: OLSEN, ET AL.
; TITLE OF INVENTION: Corpuscles of Stannius Protein, Stanniocalcin
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN

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; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/431,117A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/208,005
; FILING DATE: 8 MARCH 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: FERRARO, GREGORY D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-296
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 BASE PAIRS
; TYPE: NUCLEIC ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; MOLECULE TYPE: Oligonucleotide
US-08-431-117A-4

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Alignment Scores:
Pred. No.: 11.7 Length: 31
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.83% Indels: 0
DB: 2 Gaps: 0

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US-09-705-500A-3 (1-247) x US-08-431-117A-4 (1-31)

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Qy 241 ArgThrSerHisGluSerAla 247
Db 31 CGCACATCCCATGAGAGTGCA 11

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Search completed: June 12, 2003, 23:09:30
Job time : 107 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 12, 2003, 22:44:20 ; Search time 141 Seconds
(without alignments)
2451.672 Million cell updates/sec

Title: US-09-705-500A-3

Perfect score: 247

Sequence: 1 MLQNSAVLLVLVISASATHE.....NLRGEDSPSHKRTSHESA 247

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Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
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Searched: 870385 seqs, 699768693 residues

Word size: 1

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

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-TRANS=human40.cdi -LIST=1000 -DOCLIGN=200 -THR SCORE=quality -THR_MIN=1
-ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US09705500 @CGN 1.1.104 @runat.06062003 113647_8081
-NCPU=6 -ICPU=3 -NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCX=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60
-XGAPOP=6 -XGAPEXT=7 -XGAPOP=60 -XGAPEXT=60 -DELOP=6 -DELEXT=7

Database : Published Applications NA:

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13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:
14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	247	100.0	771	12	US-10-116-051-1
2	247	100.0	1283	10	US-09-840-989A-1
3	247	100.0	3765	12	US-10-044-090-638
4	247	100.0	3897	9	US-10-198-846-13651

Sequence 486, App
Sequence 149, App
Sequence 149, App
Sequence 149, App
Sequence 149, App
Sequence 2677, App
Sequence 33032, A
Sequence 21309, A
Sequence 4363, App
Sequence 141, App
Sequence 141, App
Sequence 141, App
Sequence 45, Appli
Sequence 398, App
Sequence 138, App
Sequence 9, Appli
Sequence 3, Appli
Sequence 72, Appl
Sequence 895, App
Sequence 23, Appl
Sequence 162, App
Sequence 399, App
Sequence 1, Appli
Sequence 5, Appli
Sequence 3, Appli
Sequence 6, Appli
Sequence 4, Appli
Sequence 7, Appli
Sequence 9, Appli
Sequence 5, Appli
Sequence 7, Appli
Sequence 7322, A
Sequence 23903, A
Sequence 12295, A
Sequence 2990, App
Sequence 3355, App
Sequence 13, Appl
Sequence 2920, App
Sequence 626, App
Sequence 8578, App
Sequence 1957, App
Sequence 6712, App
Sequence 6712, App
Sequence 6991, App
Sequence 7499, App
Sequence 125, App
Sequence 63, Appli
Sequence 7679, App
Sequence 7679, App
Sequence 9104, App
Sequence 71, Appli
Sequence 1527, App
Sequence 577, App
Sequence 1972, App
Sequence 4663, App
Sequence 2804, App
Sequence 2804, App
Sequence 3640, App
Sequence 1633, App
Sequence 8115, App
Sequence 8115, App
Sequence 767, App
Sequence 404, App
Sequence 135, App
Sequence 258, App
Sequence 11842, A
Sequence 434, App
Sequence 19660, A
Sequence 5708, App


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; CURRENT FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: PCT/US00/29432
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,740
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1283
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (45)..(788)
; OTHER INFORMATION:
; NAME/KEY: misc.feature
; LOCATION: (857)..(857)
; OTHER INFORMATION: n is equal to a, t, c, or g.
; NAME/KEY: misc.feature
; LOCATION: (1254)..(1254)
; OTHER INFORMATION: n is equal to a, t, c, or g.
; NAME/KEY: misc.feature
; LOCATION: (1279)..(1279)
; OTHER INFORMATION: n is equal to a, t, c, or g.
; US-09-840-989A-1

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Alignment Scores:		
Pred. No.:	1.99e-249	Length: 1283
Score:	247.00	Matches: 247
Percent Similarity:	100.00%	Conservative: 0
Best Local Similarity:	100.00%	Mismatches: 0
Query Match:	100.00%	Indels: 0
DB:	10	Gaps: 0

US-09-705-500A-3 (1-247) x US-09-840-989A-1 (1-1283)

Qy	1	Met	Leu	Gln	Ans	Ser	Ala	Val	Leu	Leu	Val	Leu	Val	Leu	Ser	Ala	Ser	Ala	Thr	His	Glu	20		
Db	45	ATG	CTC	CAAA	AACT	CA	GAG	AGT	GCTT	CTG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	CA	104		
Qy	21	Ala	Glu	Gln	Ans	Asp	Ser	Val	Ser	Pro	Arg	Gly	Ser	Ser	Arg	Val	Ala	Ala	Gln	Ans	Ser	Ala	40	
Db	105	GCG	GAG	CA	GAAT	GACT	CT	TG	TG	GAG	CCC	AGG	AAA	TCC	CG	AGT	GCG	GCG	CCC	AAAA	ACT	CAG	CT	164
Qy	41	Glu	Val	Val	Arg	Cys	Leu	Asn	Ser	Ala	Leu	Gln	Val	Gly	Cys	Gly	Ala	Phe	Ala	Cys	Leu	60		
Db	165	GA	GTG	GT	TG	CT	CA	CAG	TGC	CT	CA	GAG	TG	CG	CT	CA	GAG	TG	CG	CT	CG	CT	224	
Qy	61	Glu	Ans	Ser	Thr	Cys	Asp	Thr	Asp	Gly	Met	Tyr	Asp	Phe	Cys	Iys	Ser	Ser	Phe	Leu	Tyr	Ser	80	
Db	225	GA	AA	ACT	CT	CAC	CT	GT	GAC	AC	AG	TGG	AT	GAT	GAC	AT	CT	GTA	AT	CCT	CT	TG	TG	284
Qy	81	Ala	Ala	Val	Ser	Phe	Asp	Thr	Gln	Gly	Ala	Phe	Val	Lys	Glu	Ser	Leu	Lys	Cys	Ile	Ala	100		
Db	285	GCT	GT	CT	AA	TT	TGA	CAC	T	CAG	GGA	AA	GCA	T	CT	G	CA	A	G	AG	CT	T	AA	344
Qy	101	Asn	Gly	Val	Thr	Ser	Lys	Val	Phe	Leu	Ala	Ile	Arg	Arg	Cys	Ser	Thr	Phe	Gln	Arg	Met	120		
Db	345	AC	G	G	G	G	T	CAC	T	CC	CA	A	G	GT	CT	T	CT	CC	CA	AT	CG	G	AG	404
Qy	121	Ile	Ala	Glu	Val	Gln	Glu	Cys	Tyr	Ser	Lys	Leu	Asn	Val	Cys	Ser	Ile	Ala	Lys	Arg	140			
Db	405	ATT	GT	G	AG	TG	TG	CA	GGA	AG	TG	CT	TAC	AG	CA	AG	CT	GAA	T	GT	TG	TG	CA	464
Qy	141	Asn	Pro	Glu	Ala	Ile	Thr	Glu	Val	Val	Gln	Leu	Pro	Ans	His	Phe	Ser	Ans	Arg	Tyr	Tyr	160		
Db	465	AA	CC	CT	G	AG	CC	AT	CAC	T	CA	G	T	CG	CT	CG	CC	CA	AT	CAC	T	TT	CT	524
Qy	161	Asn	Arg	Leu	Val	Arg	Ser	Leu	Leu	Glu	Cys	Asp	Glu	Asp	Thr	Val	Ser	Thr	Ile	Arg	Asp	180		
Db	525	AA	CA	GAC	TT	G	CC	GA	AG	CT	CT	G	TA	T	GT	GAT	GA	AG	CA	GAC	AT	CA	584	
Qy	181	Ser	Leu	Met	Glu	Lys	Ile	Gly	Pro	Ans	Met	Ala	Ser	Leu	Phe	His	Ile	Leu	Gln	Thr	Asp	200		

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Db      585 AGCTGTATGGAGAAAATGGGCCCTTAACATGGCCAGCCTCTTCCACATCTCTGCAGACAGAC 644
Qy      201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgAlaArgThrAsnGluProGln 220
Db      645 CACTGTGCCAAACACACCCACGAGCTGACTTCAACAGAGACGACCACTGAGCCGCAG 704
Qy      221 LysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHisIleLys 240
Db      705 AAGCTGAAGTCTCTCCAGGAACCTCCGAGGTGAGGAGGACTCTCCCTCCCACATCAAA 764
Qy      241 ArgThrSerHisGluSerAla 247
Db      765 CGCACATCCCATGAGAGTGCA 785

RESULT 3
US-10-044-090-638
; Sequence 638, Application US/10044090
; Patent No. US20020137081A1
; GENERAL INFORMATION:
; APPLICANT: Olga Bandman
; TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
; FILE REFERENCE: PA-0028 US
; CURRENT APPLICATION NUMBER: US/10/044,090
; CURRENT FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 850
; SOFTWARE: PERL Program
; SEQ ID NO 638
; LENGTH: 3765
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: incyte ID No. US20020137081A1 331181.1
; NAME/KEY: unsure
; LOCATION: 2378, 3184, 3187, 3194
; OTHER INFORMATION: a, t, c, g, or other
US-10-044-090-638

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Alignment Scores:	
Pred. No.:	5.6e-249
Score:	247.00
Percent Similarity:	100.0%
Best Local Similarity:	100.0%
Query Match:	100.0%
DB:	12
Length:	3765
Matches:	247
Conservative:	0
Mismatches:	0
Indels:	0
Gaps:	0

US-09-705-500A-3 (1-247) x US-10-044-090-638 (1-3765)

Qy	1	MetLeuGlnAsnSerAlaValLeuLeuValLeuValIleSerAlaSerAlaThrHisGlu	20
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Db	234	CGCGAGCAGAAATGACTCTGTGAGCCCGAGGAATCCCGAGTGGCGGCTCAAAACATCAGCT	293
Qy	41	GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu	60
Db	294	GAGTGGTTCGTTGCCCTCAACAGTGCTCTACAGGTGGCTCGGGGCTTTTCATGCCCTG	353
Qy	61	GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer	80
Db	354	GAAACTCCACCTGTGACACAGATGGGATGATGACATCTGTAAATCCTCTTTGTACAGC	413
Qy	81	AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAla	100
Db	414	GCTGCTAAATTTTGACATTCAGGGGAAAAGCATTCGTCAAGAGAGAGCTTAAAAATGCATCGCC	473
Qy	101	AsnGlyValThrSerLysValPheLeuAlaIleArgCysSerThrPheGlnArgMet	120
Db	474	AACGGGTACCTTCAAGGTCTTCTCGCCATTCGGAGGTGCTCACTTTCAAAGGATG	533

QY 121 IleAlaGluValGlnGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
 DB 534 ATTGCTAGGTCAGGAAAGTGTACAGCAAGCTGAATGTGTGAGCATGCCAAGCGG 593
 QY 141 AsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
 DB 594 AACCCCTGAAGCCATCACTGAGTGTCTCCAGCTGCCCAATCACTTCTCCAACAGATACTAT 653
 QY 161 AsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp 180
 DB 654 AACAGACTTGTCCGAAGCCCTGGAATGTGTGATGAGACACAGCTCAGCAATCAGAGAC 713
 QY 181 SerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
 DB 714 AGCCTGATGGAGAAATTTGGGCTTAACATGGCCAGCCTCTTCCATCTCGCAGACAGAC 773
 QY 201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgThrAsnGluProGln 220
 DB 774 CACTGTGCCCAACACACCACGAGCTGACTTTCAACAGGAGACGCCCAATGAGCCGCGAG 833
 QY 221 LysLeuValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHisIleLys 240
 DB 834 AAGCTGAAAGTCTCTCTAGGAACCTCCGAGGTGAGGAGACTCTCCCTCCACATCAAA 893
 QY 241 ArgThrSerHisGluSerAla 247
 DB 894 CGCACATCCCATGAGAGTGCA 914

RESULT 4

US-10-198-846-13651
 ; Sequence 13651, Application US/10198846
 ; Publication No. US2003009974A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lillie, James
 ; APPLICANT: Xu, Yongyao
 ; APPLICANT: Wang, Youzhen
 ; APPLICANT: Steinmann, Kathleen
 ; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
 ; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
 ; TITLE OF INVENTION: THERAPY OF BREAST CANCER
 ; FILE REFERENCE: MRI-049
 ; CURRENT APPLICATION NUMBER: US/10/198,846
 ; CURRENT FILING DATE: 2002-07-18
 ; PRIOR APPLICATION NUMBER: 60/306,220
 ; PRIOR FILING DATE: 2001-07-18
 ; NUMBER OF SEQ ID NOS: 14084
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 13651
 ; LENGTH: 3897
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: 3878, 3879, 3880, 3881, 3882, 3883, 3884, 3885, 3886, 3887,
 ; LOCATION: 3888, 3889, 3890, 3891, 3892, 3893, 3894, 3895, 3896, 3897
 ; OTHER INFORMATION: n = A,T,C or G
 US-10-198-846-13651

Alignment Scores:

Pred. No.: 5,79e-249 Length: 3897
 Score: 247.00 Matches: 247
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0

US-09-705-500A-3 (1-247) x US-10-198-846-13651 (1-3897)

QY 1 MetLeuGlnAsnSerAlaValLeuLeuValLeuValIleSerAlaSerAlaThrHisGlu 20
 DB 285 ATGCTCCAAAATCAGCAGTGTCTTGTGCTGGTGATGATGCTCTGCAACCATGAG 344
 QY 21 AlaGluGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40

DB 345 CGGAGCAGAAATGACTCTGTGAGCCCCAGGAAATCCCGAGTGGCGGCTCAAAACTCAGCT 404
 QY 41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
 DB 405 GAAGTGGTTCGTTCCTCAACAGTGTCTACAGGTGGCTCGGGGCTTTTGCATGCGCTG 464
 QY 61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
 DB 465 GAAACTCCACCTGTGACACAGATGGGATGTATGACATCTCTAAATCTCTCTGTGTACAGC 524
 QY 81 AlalaLysPheAspThrGlnGlyAlaPheValLysGluSerLeuLysCysIleAla 100
 DB 525 GCTGCTAAATTTGACACTCAGGAAAGACATTCGTCAAAGAGAGACTTAAATAATGATCGCC 584
 QY 101 AsnGlyValThrSerLysValPheLeuAlaIleArgCysSerThrPheGluArgMet 120
 DB 585 AACGGGTGCTCTCAAGTCTTCTCGCCATTCGAGGTGCTCCACTTTCCAAGGATG 644
 QY 121 IleAlaGluValGlnGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
 DB 645 ATTGCTGAGGTGCAGGAGAGCTGTACAGCAAGCTGAATGTGTGAGCATGCCAAGCGG 704
 QY 141 AsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
 DB 705 AACCTGAAGCCATCACTGAGTGTCTCCAGCTGCCCAATCACTTCTCCACAGATACTAT 764
 QY 161 AsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp 180
 DB 765 AACAGACTTGTCCGAAGCCTGCTGGAATGTGTGATGAGACACAGCTCAGCAATCAGAGAC 824
 QY 181 SerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
 DB 825 AGCCTGATGAGAAATTTGGGCTTAACATGCGCCAGCCTCTTCCACATCTCTCAGACAGAC 884
 QY 201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgThrAsnGluProGln 220
 DB 885 CACTGTGCCCCAAACACACCCACGAGCTGACTTCAACAGGAGACGCCCAATGAGCCGCGAG 944
 QY 221 LysLeuValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHisIleLys 240
 DB 945 AAGCTGAAAGTCTCTCCAGGAACCTCCGAGGTGAGGAGGACTCTCTCCCTCCACATCAAA 1004
 QY 241 ArgThrSerHisGluSerAla 247
 DB 1005 CGCACATCCCATGAGAGTGCA 1025

RESULT 5

US-09-925-300-486
 ; Sequence 486, Application US/09925300
 ; Patent No. US20020151681A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Craig Rosen,
 ; APPLICANT: Steve Ruben
 ; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
 ; FILE REFERENCE: PA101
 ; CURRENT APPLICATION NUMBER: US/09/925,300
 ; CURRENT FILING DATE: 2001-08-10
 ; PRIOR APPLICATION NUMBER: PCT/US00/05988
 ; PRIOR FILING DATE: 2000-03-08
 ; PRIOR APPLICATION NUMBER: 60/124,270
 ; PRIOR FILING DATE: 1999-03-12
 ; NUMBER OF SEQ ID NOS: 1890
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 486
 ; LENGTH: 2572
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (823)
 ; OTHER INFORMATION: n equals a,t,g, or c
 US-09-925-300-486


```

; APPLICANT: Wang, TongTong
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.491C5
; CURRENT APPLICATION NUMBER: US/09/778.320
; CURRENT FILING DATE: 2001-02-06
; NUMBER OF SEQ ID NOS: 301
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 149
; LENGTH: 585
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(585)
; OTHER INFORMATION: n=A,T,C or G
US-09-778-320-149

Alignment Scores:
Pred. No.: 1.49e-158 Length: 585
Score: 160.00 Matches: 160
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 64.78% Indels: 0
DB: 10 Gaps: 0

US-09-705-500A-3 (1-247) x US-09-778-320-149 (1-585)

Qy 88 GlyLysAlaPheValLysGluSerLeuLysCysIleAlaAsnGlyValThrSerLysVal 107
Db 33 GGAAGAAGCATTCGTCNAAAGAGAGCTTAAATTCATCGCCAACGGGGTCACCTCCAAAGGTC 92
Qy 108 PheLeuAlaIleArgArgCysSerThrPheGlnArgMetIleAlaGluValGlnGluGlu 127
Db 93 TTCTCTGCCATTTCGAGGTGCTCCACTTTCNAAAGGATGATTGCTGAGGTGCAGGAGAG 152
Qy 128 CysTyrSerLysLeuAsnValCysSerIleAlaLysArgAsnProGluAlaIleThrGlu 147
Db 153 TGCTACAGCAAGCTGAATGTGTGCAGCATCGCCAAAGCGAACCTGAAGCCATCACTGAG 212
Qy 148 ValValGlnLeuProAsnHisPheSerAsnArgTyrTyrAsnArgLeuValArgSerLeu 167
Db 213 GTCTGTCAGGTGCCCAATCACTTCTCAACACAGATACTATAACAGACTTGTGCCAAGCCTG 272
Qy 168 LeuGluCysAspGluAspThrValSerThrIleArgAspSerLeuMetGluLysIleGly 187
Db 273 CTGGAATGTGATGAAGACACACAGTCAGCACAAATCAGACAGACGCTGATGAGAAAAATTGG 332
Qy 188 ProAsnMetAlaSerLeuPheHisIleLeuGlnThrAspHisCysAlaGlnThrHisPro 207
Db 333 CCTAACATGCCAGCCTCTTCCACATCCTGCAGACAGACCACTGTGCCCAACACACACCA 392
Qy 208 ArgAlaAspPheAsnArgArgArgThrAsnGluProGlnLysLeuLysValLeuLeuArg 227
Db 393 CGAGCTGACTTCAACAGGAGACGCACCAATGAGCGCGAAGAGCTGAAAGTCTCTCTCAG 452
Qy 228 AsnLeuArgGlyGluGluAspSerProSerHisIleLysArgThrSerHisGluSerAla 247
Db 453 AACCTCGAGGTGAGGAGGACTTCTCTTCCACATCAACGCACATCCCATGAGAGTGCA 512

RESULT 7
US-09-910-689-149
; Sequence 149, Application US/09910689
; Patent No. US20020081609A1
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Day, Craig H.
; APPLICANT: Jiang, Yugu
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Wang, Tongtong
; APPLICANT: McNeill, Patricia D.

```



```

; APPLICANT: Jiang, Yugu
;
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; OF PANCREATIC CANCER
;
; FILE REFERENCE: 210121-566
;
; CURRENT APPLICATION NUMBER: US/10/060,036
;
; CURRENT FILING DATE: 2002-01-30
;
; NUMBER OF SEQ ID NOS: 4560
;
; SOFTWARE: FastSeq for Windows Version 4.0
;
; SEQ ID NO 2677
;
; LENGTH: 473
;
; TYPE: DNA
;
; ORGANISM: Homo sapiens
;
US-10-060-036-2677

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Alignment Scores:			
Pred. No.:	2,738-129	Length:	473
Score:	132.00	Matches:	132
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	53.44%	Indels:	0
DB:	9	Gaps:	0

US-09-705-500A-3 (1-247) x US-10-060-036-2677 (1-473)

116	ThrPheGlnArgMetIleAlaGlnValGlnGluGluCysTyrSerLysLeuAsnValCys	135
472	ACTTTCCAAAGGATGATTCTGAGGTGCAGGAAGAGTGTACAGCAAGCTGAATGTGTGC	413
136	SerIleAlaLysArgAsnProGluAlaIleThrGluValValGlnLeuProAsnHisPhe	155
412	AGCATCGCCAAAGCGAACCCTGAAGCCATCACTGAGGTGTCGACGTGCCCAATCACTTC	353
156	SerAsnArgTyrTyrAsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrVal	175
352	TCCAACAGATACTATAACAGAGCTTGCCGAGAGCTGTGGNATGTGATGAAGACACAGTC	293
176	SerThrIleArgAspSerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHis	195
292	AGCAACAATCAGACAGACGCTGATGAGAGAAATTGGGGCTTAACATGGCGACGCTTCCAC	233
196	IleLeuGlnThrAspHisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgArg	215
232	ATCTTCGACAGACAGACCTGTGGCCCAACACACCCAGAGCTGACTTCAACAGGAGACGC	173
216	ThrAsnGluProGlnLysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSer	235
172	ACCAATGAGCGCAGAGCTGAAAGTCTCTCTCAGGAACCTCCGAGGTGAGGAGGACTCT	113
236	ProSerHisIleLysArgThrSerHisGluSerAla	247
112	CCCTCCCAACATCAAAACGACATCCCATGAGAGTGCA	77

```

RESULT 10
US-09-918-995-33032
; Sequence 33032, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 204111-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 33032
; LENGTH: 436
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-995-33032

```

Alignment Scores:		1.28e-70	Length:	436
Pred. No.:	Score:	76.00	Matches:	76
Percent Similarity:		100.00%	Conservative:	0
Best Local Similarity:		100.00%	Mismatches:	0
Query Match:		30.77%	Indels:	0
DB:		9	Gaps:	0

US-09-705-500A-3 (1-247) x US-09-918-995-33032 (1-436)

Qy	172	GluAspThrValSerThrIleArgAspSerLeuMetGluLysIleGlyProAsnMetAla	191
Db	2	GAAGACACAGTCAGCACCAATCAGAGACACGCTGTATGGAGAAAATTGGGCTTAAACATGGCC	61
Qy	192	SerLeuPheHisIleLeuGlnThrAspHisCysAlaGlnThrHisProArgAlaAspPhe	211
Db	62	AGCTCTTCCACATCCTGCGACAGACACCACTGTGCCCAACACACCCAGAGCTGACTTC	121
Qy	212	AsnArgArgArgThrAsnGluProGlnLysLeuLysValLeuLeuArgAsnLeuArgGly	231
Db	122	AACAGGAGAGCGACCAATGAGCCGACAGAAGCTGAAAGTCTCTCTCAGGAACCTCCGAGGT	181
Qy	232	GluGluAspSerProSerHisIleLysArgThrSerHisGluSerAla	247
Db	182	GAGGAGAGACTCTCCTCCCATCAAAACGCACATCCCATGAGAGTGCA	229

RESULT 11

US-09-864-761-21309/c
: Sequence 21309, Application US/09864761
: Patent NO. US20020048763A1
: GENERAL INFORMATION:
: APPLICANT: Penn, Sharron G.
: APPLICANT: Rank, David R.
: APPLICANT: Hanzel, David K.
: APPLICANT: Chen, Wensheng
: TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
: FILE REFERENCE: Aescmica-X-1
: CURRENT APPLICATION NUMBER: US/09/864,761
: CURRENT FILING DATE: 2001-05-23
: PRIOR APPLICATION NUMBER: US 60/180,312
: PRIOR FILING DATE: 2000-02-04
: PRIOR APPLICATION NUMBER: US 60/207,456
: PRIOR FILING DATE: 2000-05-26
: PRIOR APPLICATION NUMBER: US 09/632,366
: PRIOR FILING DATE: 2000-08-03
: PRIOR APPLICATION NUMBER: GB 24263.6
: PRIOR FILING DATE: 2000-10-04
: PRIOR APPLICATION NUMBER: US 60/236,359
: PRIOR FILING DATE: 2000-09-27
: PRIOR APPLICATION NUMBER: PCT/US01/00666
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00667
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00664
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00669
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00665
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00668
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00663
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00662
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00661
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00670
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: US 60/234,687
: PRIOR FILING DATE: 2000-09-21
: PRIOR APPLICATION NUMBER: US 09/608,408

;; PRIOR FILING DATE: 2000-06-30
;; PRIOR APPLICATION NUMBER: US 09/774,203
;; PRIOR FILING DATE: 2001-01-29
;; NUMBER OF SEQ ID NOS: 49117
;; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
;; SEQ ID NO 21309
;; LENGTH: 219
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: MAP TO AC012119.1
;; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.7
;; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 2.4
;; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.8
;; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.8
;; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.4
;; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.1
;; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.8
;; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.7
;; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.2
;; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.7
;; OTHER INFORMATION: SWISSPROT HIT: P52823, EVALUE 2.00e-36
;; OTHER INFORMATION: NT HIT: AF098463.1, EVALUE 1.00e-120
;; OTHER INFORMATION: EST_HUMAN HIT: AW954342.1, EVALUE 1.00e-116
US-09-864-761-21309

Alignment Scores:
Pred. No.: 1,03e-66 Length: 219
Score: 72.00 Matches: 72
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 29.15% Indels: 0
DB: 10 Gaps: 0

US-09-705-500A-3 (1-247) x US-09-864-761-21309 (1-219)

Qy 88 GlyLysAlaPheValIysGluSerLeuLysCysIleAlaAsnGlyValThrSerLysVal 107
Db 219 GAAAGAGATTCTGTCAGAGAGCTTAAATGCATCGCCAGGGGTCACTCCCAAGGTC 160
Qy 108 PheLeuAlaIleArgArgCysSerThrPheGlnArgMetIleAlaGluValGlnGlu 127
Db 159 TTCTCGCCATTTCGGAGGTGCTCCACTTTCCAAAGGATGATTGCTGAGGTGCAGGAAG 100
Qy 128 CysTyrSerLysLeuAsnValCysSerIleAlaLysArgAsnProGluAlaIleThrGlu 147
Db 99 TCTACAGCAAGCTGATGTGTGCAGCATCGCCAGCGAACCTTGAGCCCATCTGAG 40
Qy 148 ValValGlnLeuProAsnHisPheSerAsnArgTyr 159
Db 39 GTCTGTCAGTCCCAATCACTTCTCCACAGGTAC 4

RESULT 12

US-09-864-761-4563/c
; Sequence 4563, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:

;; APPLICANT: Penn, Sharon G.
;; APPLICANT: Rank, David R.
;; APPLICANT: Hanzel, David K.
;; APPLICANT: Chen, Wensheng
;; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
;; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
;; FILE REFERENCE: Aomics-X-1
;; CURRENT APPLICATION NUMBER: US/09/864, 761
;; CURRENT FILING DATE: 2001-05-23
;; PRIOR APPLICATION NUMBER: US 60/180, 312
;; PRIOR FILING DATE: 2000-02-04
;; PRIOR APPLICATION NUMBER: US 60/207, 456
;; PRIOR FILING DATE: 2000-05-26
;; PRIOR APPLICATION NUMBER: US 09/632, 366
;; PRIOR FILING DATE: 2000-08-03
;; PRIOR APPLICATION NUMBER: GB 24263.6

;; PRIOR FILING DATE: 2000-10-04
;; PRIOR APPLICATION NUMBER: US 60/236, 359
;; PRIOR FILING DATE: 2000-09-27
;; PRIOR APPLICATION NUMBER: PCT/US01/006666
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/006667
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/006664
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/006669
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/006665
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/006668
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/006663
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/006662
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/006661
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/006670
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: US 60/234, 687
;; PRIOR FILING DATE: 2000-09-21
;; PRIOR APPLICATION NUMBER: US 09/608, 408
;; PRIOR FILING DATE: 2000-06-30
;; PRIOR APPLICATION NUMBER: US 09/774, 203
;; NUMBER OF SEQ ID NOS: 49117
;; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
;; SEQ ID NO 4563
;; LENGTH: 362
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: MAP TO AC012119.1
;; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.7
;; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 2.4
;; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.8
;; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.8
;; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.4
;; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.8
;; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.1
;; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.7
;; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.2
;; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.7
US-09-864-761-4563

Alignment Scores:
Pred. No.: 5,26e-34 Length: 362
Score: 41.00 Matches: 41
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 16.60% Indels: 0
DB: 10 Gaps: 0

US-09-705-500A-3 (1-247) x US-09-864-761-4563 (1-362)

Qy 119 ArgMetIleAlaGluValGlnGluCysTyrSerLysLeuAsnValCysSerIleAla 138
Db 361 AGGATGATTGCTGAGGTGCAGGAAGAGTGTACAGCAAGCTGAATGTGTGCAGCATCGCC 302
Qy 139 LysArgAsnProGluAlaIleThrGluValGlnLeuProAsnHisPheSerAsnArg 158
Db 301 AAGCGGAACCCCTGAAGCCATCACTGAGGTCTGCCAGTGCCTTCTCCACAGG 242
Qy 159 Tyr 159
Db 241 TAC 239
RESULT 13
US-09-778-320-141

```

; OTHER INFORMATION: n = A,T,C or G
US-09-910-689-141

Alignment Scores:
Pred. No.: 6.78e-33 Length: 420
Score: 40.00 Matches: 40
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 16.19% Indels: 0
DB: 10 Gaps: 0

US-09-705-500A-3 (1-247) x US-09-910-689-141 (1-420)
QY 95 SerLeuLysCysIleAlaAsnGlyValThrSerLysValPheLeuAlaIleArgArgCys 114
Db 31 AGCTTAAATGATCGCCACACGGGGTCACTCCAAAGGTCTTCTCGCCATTCCGAGGTGC 90
QY 115 SerThrPheGlnArgMetIleAlaGluValcInGluCysTyrSerLysLeuAsnVal 134
Db 91 TCCACTTTCCAAAGATGATTGTGAGGTGCGAAGAGTGTACAGCAAGCTGGAATGTG 150

RESULT 15
US-10-010-742-141
; Sequence 141, Application US/10010742
; Patent No. US20020146727A1
; GENERAL INFORMATION:
; APPLICANT: Dillion, Davin C.
; APPLICANT: Day, Craig H.
; APPLICANT: Jiang, Yugu
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Wang, Tongtong
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Bennington, Angela Ann
; APPLICANT: Zehentner, Barbara
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.491C7
; CURRENT APPLICATION NUMBER: US/10/010,742
; CURRENT FILING DATE: 2001-11-30
; NUMBER OF SEQ ID NOS: 307
; SOFTWARE: FastSQ for Windows Version 4.0
; SEQ ID NO 141
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; LOCATION: 20, 21, 23, 28, 155, 174, 221, 239, 240, 258, 265, 302, 307,
; LOCATION: 316, 342, 346, 374, 387, 388, 402, 418
; OTHER INFORMATION: n = A,T,C or G
US-10-010-742-141

Alignment Scores:
Pred. No.: 6.78e-33 Length: 420
Score: 40.00 Matches: 40
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 16.19% Indels: 0
DB: 12 Gaps: 0

US-09-705-500A-3 (1-247) x US-10-010-742-141 (1-420)
QY 95 SerLeuLysCysIleAlaAsnGlyValThrSerLysValPheLeuAlaIleArgArgCys 114
Db 31 AGCTTAAATGATCGCCACACGGGGTCACTCCAAAGGTCTTCTCGCCATTCCGAGGTGC 90
QY 115 SerThrPheGlnArgMetIleAlaGluValcInGluCysTyrSerLysLeuAsnVal 134
Db 91 TCCACTTTCCAAAGATGATTGTGAGGTGCGAAGAGTGTACAGCAAGCTGGAATGTG 150

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Search completed: June 12, 2003, 23:59:16
Job time : 164 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 12, 2003, 21:52:10 ; Search time 1418 Seconds
(without alignments)
2821.076 Million cell updates/sec

Title: US-09-705-500A-3

Perfect score: 247

Sequence: 1 MLQNSVLLVLIVISASATHE.....NLGRGEEDSPSHIKTSHESA 247

Scoring table: OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Zgapop 6.0 , Zgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 16154066 seqs, 8097743376 residues

Word size: 1

Total number of hits satisfying chosen parameters: 32308016

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Command line parameters: -MODEL=frame+ p2n.model -DEV=xlp
-O=/cgn2_1/USPTO_spool/US09705500/runat_06062003_113645_7987/app_query.fasta_1.391
-DB=EST -OFMT=fasta -SUFFIX=oligo -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi -LIST=1000
-DOCLALIGN=200 -THR SCORE=quality -THR MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc
-NORW=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09705500@cgn 1 1 1525 @runat_06062003_113645_7987 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_estl:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_nam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	228	92.3	869	14	BQ672018	BQ672018 AGENCOURT
2	208	84.2	1057	14	BQ225453	BQ225453 AGENCOURT
3	207	83.8	648	13	BM311682	BM311682 ig60f04.x
4	205	83.0	617	13	BM311087	BM311087 ig60f04.y
5	199	80.6	644	10	AW965863	AW965863 EST377936
6	168	68.0	646	10	AW954342	AW954342 EST377936
7	168	68.0	915	14	BQ894224	BQ894224 AGENCOURT
8	156	63.2	782	9	AL549427	AL549427 AL549427
9	135	54.7	577	14	BQ308414	BQ308414 MRO-BT450
10	122	49.4	907	9	AU122680	AU122680 AU122680
11	118	47.8	1010	14	BM924595	BM924595 AGENCOURT
12	105	42.5	619	13	BI010260	BI010260 MR2-EN009
13	103	41.7	605	13	BI010412	BI010412 MR2-EN009
14	99	40.1	483	14	R72337	R72337 Y189D08.r1
15	95	38.5	437	10	AW996662	AW996662 QV3-BN004
16	95	38.5	543	14	BQ636799	BQ636799 he01f01.y
17	90	36.4	524	14	BM708153	BM708153 UI-E-C11-
18	86	34.8	513	10	BE476621	BE476621 159962 BA
19	86	34.8	543	9	AL702795	AL702795 DKF2p686H
20	86	34.8	560	12	BF042539	BF042539 BP250022A
21	85	34.4	908	9	AL550611	AL550611 AL550611
22	84	34.0	739	9	AI115911	AI115911 ue96d011.y
23	83	33.6	930	12	BF303368	BF303368 602030289
24	81	32.8	366	14	R73246	R73246 Y109F01.r1
25	80	32.4	412	14	R48681	R48681 Y765B07.r1
26	76	30.8	375	14	BM720350	BM720350 UI-E-E30-
27	72	29.1	301	9	AA297962	AA297962 EST113548
28	71	28.7	422	10	AW784374	AW784374 z61h07.g
29	69	27.9	623	13	BI081334	BI081334 602879386
30	68	27.5	251	13	BI975654	BI975654 484119 MA
31	66	26.7	915	13	BI182587	BI182587 UNL-P-FN-
32	63	25.5	473	9	AL710960	AL710960 DKF2p686A
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35	44	17.8	530	12	BF854554	BF854554 MR2-EN009
36	36	14.6	414	9	AI621151	AI621151 tu88a10.x
37	31	12.6	189	9	AA297965	AA297965 EST113551
38	30	12.1	719	13	BI764976	BI764976 603051122
39	29	11.7	132	10	AW365317	AW365317 MRO-HT006
40	29	11.7	555	9	AI022950	AI022950 ow68908.s
41	28	11.3	461	10	AW463836	AW463836 BP230013B
42	27	10.9	417	12	BF849408	BF849408 QVA-EN009
43	26	10.5	563	10	BB856959	BB856959 BB856959
44	24	9.7	774	13	BI181756	BI181756 603179881
45	21	8.5	250	17	AZ754534	AZ754534 CQ1b02.f
46	21	8.5	636	14	BM946297	BM946297 UI-M-EMO-
47	19	7.7	388	10	BE491299	BE491299 db71b12.y
48	18	7.3	513	14	BM678748	BM678748 UI-E-E30-
49	18	7.3	516	12	BE912013	BE912013 601662782
50	18	7.3	879	13	BI769460	BI769460 603054789
51	17	6.9	879	13	BI769460	BI769460 603054789
52	16	6.5	384	12	BF043835	BF043835 BP250014A
53	14	5.7	240	10	BB571047	BB571047 BB571047
54	12	4.9	350	13	BI359723	BI359723 384376 MA
55	12	4.9	781	17	CNS03TU4	AL260293 Tetradon
56	11	4.5	485	12	BF431257	BF431257 To10d04.x
57	11	4.5	566	13	BI184757	BI184757 UNL-P-FN-
58	9	3.6	139	10	AV985696	AV985696 AV985696
59	9	3.6	164	10	AV681234	AV681234 AV681234
60	9	3.6	308	10	AV990834	AV990834 AV990834
61	9	3.6	338	10	AV986761	AV986761 AV986761
62	9	3.6	375	10	AV952436	AV952436 AV952436
63	9	3.6	385	9	AJ494038	AJ494038 AJ494038
64	9	3.6	411	10	AV991042	AV991042 AV991042


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c 985 7 2.8 322 17 A2502532
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c 987 7 2.8 323 13 B1172943
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c 993 7 2.8 325 9 A1427315
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c 995 7 2.8 325 10 BB502430
c 996 7 2.8 325 12 BG021440
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c 998 7 2.8 326 10 BE525434
c 999 7 2.8 327 9 A1278915
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ALIGNMENTS

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RESULT 1
BQ672018 869 bp mRNA linear EST 15-JUL-2002
LOCUS BQ672018.1 GI:21782852
DEFINITION AGENCOURT 8032625 NIH_MGC_102 Homo sapiens cDNA clone IMAGE:6213518
5', mRNA sequence.
ACCESSION BQ672018
VERSION BQ672018.1
KEYWORDS EST.
SOURCE human.

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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 869)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LICM2379 row: f column: 15
High quality sequence stop: 673.
FEATURES
Location/Qualifiers
1..869
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6213518"
/tissue_type="epidermoid carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: salivary gland; Vector: pOTB7; Site: 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Library constructed
by Ling Hong in the laboratory of Gerald M. Rubin
(University of California, Berkeley) using ZAP-cDNA
synthesis kit (Stratagene) and Superscript II RT (Life
Technologies). Note: this is a NIH-MGC Library."
BASE COUNT 234 a 231 c 214 g 188 t
ORIGIN
Alignment Scores:
Pred. No.: 2,56e-218 Length: 869
Score: 228.00 Matches: 228
Percent Similarity: 100.00% Conservativeness: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 92.31% Indels: 0
DB: 14 Gaps: 0
US-09-705-500A-3 (1-247) x BQ672018 (1-869)
Qy 1 MetLeuGlnAsnSerAlaValLeuValLeuValSerAlaSerAlaThrHisGlu 20
Db 21 ATGCTCCAAACTCAGCAGTCTTCTGCTGTGTGATCAGTGTCTTCTGCAACCATGAG 80
Qy 21 AlaGluGlnAspSerValSerProArglySerArgValAlaAlaGlnAsnSerAla 40
Db 81 GCGGAGCAGATGATCTGTGAGCCCGAGGAAATCCCGAGTGGCGGTCAAAATCAGCT 140
Qy 41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
Db 141 GAATGGTTCGTTCCCTCAACAGTCTTACAGTTCGGCTCGGGGGCTTTTCATGCTG 200
Qy 61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysIleCysSerPheLeuTyrSer 80
Db 201 GAAATCTCCACTGTGACACAGATGGGATGTATGACATCTGTAATCTCTTCTGTACAGC 260
Qy 81 AlaAlaLysPheAspThrGlnGlyAlaPheValLysGluSerLeuValCysIleAla 100
Db 261 GCTCTAAATTTGACATCACTGAGGAAAGAGCATTCCTCAAGAGAGACTTAAATATGATCGCC 320
Qy 101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
Db 321 AACGGGGTCACTTCAAGGTCTTCTCGCCATTCGGAGGTGCTCCACTTCCAAAGGATG 380
Qy 121 IleAlaGluValGlnGluCysTyrSerIleLysLeuAsnValCysSerIleAlaLysArg 140

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Db      381 ATTGCTGAGTCCAGAGAGAGTGTACAGCAAGCTGAATGTGTGAGCATGCCAAGCGG 440
Qy      141 AsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
Db      441 AACCTGGAAGCCATCACTGAGGTGCTCCAGCTGCCCAATCACTTCTCCACAGATACTAT 500
Qy      161 AsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp 180
Db      501 AACAGACTTGTCCGAAGCCTGCTGGAATGTGATGAAGACACAGCAGTCCAGCAATCAGAG 560
Qy      181 SerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
Db      561 AGCCTGATGGAGAAATTTGGCCTTAACATGGCCAGCTTCCACATCTCGCAGACAGAC 620
Qy      201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgThrAsnGluProGln 220
Db      621 CACTGTGCCCAACACACCCAGCTGACTTCAACAGGAGAGCGCAACCAATGAGCGGAG 680
Qy      221 LysLeuLysValLeuLeuArgAsn 228
Db      681 AAGCTGAAAGTCTCTCTCAGGAAC 704

RESULT 2
LOCUS   BQ225453 1057 bp mRNA linear EST 02-MAY-2002
DEFINITION AGENCOURT_7257225 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:5773821
5', mRNA sequence.
ACCESSION BQ225453
VERSION BQ225453.1 GI:20406853
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1057)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12842 row: e column: 22
High quality sequence stop: 578.
FEATURES
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1..1057
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:5773821"
/clone_lib="NIH_MGC_68"
/tissue_type="large cell carcinoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lung; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.8 Kb. Library constructed by Life
Technologies."
BASE COUNT 291 a 293 c 219 g 254 t
ORIGIN
Alignment Scores:
Pred. No.: 3,828-198 Length: 1057
Score: 208.00 Matches: 208
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 84.21% Indels: 0
DB: 14 Gaps: 0
US-09-705-500A-3 (1-247) x BQ225453 (1-1057)

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Qy      40 AlaGluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCys 59
Db      4 GCTGAAGTGGTGTGCTGCTCAACAGTGTCTACAGGTGGCTGCGGGGCTTTTCATGCG 63
Qy      60 LeuGluAsnSerThrCysAspThrAspClyMetTyrAspIleCysLysSerPheLeuTyr 79
Db      64 CTGAAATCTCCACTGTCAGACAGATGGGATGTATGACATCTGTAAATCTCTTCTTGAC 123
Qy      80 SerAlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIle 99
Db      124 AGCGCTGCTAAATTTGACACTCAGGGAAGAGCATTCGTCAAAGAGAGAGCTTAAATGTCATC 183
Qy      100 AlaAsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArg 119
Db      184 GCCAAGGGGGTCACTCTCAAGGTCTTCTCGCCATTCGAGGTGCTCCACTTTCCAAAGG 243
Qy      120 MetIleAlaGluValGlnGluCysTyrSerLysLeuAsnValCysSerIleAlaLys 139
Db      244 ATGATTGCTGAGGTGCAGGAAGAGTGTACAGCAAGCTGAATGTGTGAGCATGCCCAAG 303
Qy      140 ArgAsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyr 159
Db      304 CGGAACCTCGAAGCCATCACTGAGGTGCTCCAGCTGCCCAATCACTTCTCCACAGATAC 363
Qy      160 TyrAsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArg 179
Db      364 TATAACAGACTTGTCCGAAGCCTGCTGGAATGTGATGAAGACACAGTCAGCAATCAGA 423
Qy      180 AspSerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThr 199
Db      424 GACAGCCTGATGGAGAAATTTGGGCCTTAACATGGCCAGCTTCTCCACATCTCGCAGACA 483
Qy      200 AspHisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgThrAsnGluPro 219
Db      484 GACCACCTGTGCCCAACACACCCAGCAGTCACTTCAACAGGAGAGCGCACCAATGAGCGG 543
Qy      220 GlnLysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHisIle 239
Db      544 CAGAAGCTGAAAGTCTCTCTCAGGAACCTCCGAGGTGAGGAGGACTCTCCCTCCACATC 603
Qy      240 LysArgThrSerHisGluSerAla 247
Db      604 AAACGCACATCCCATGAGAGTGCA 627

RESULT 3
LOCUS   BM311682 648 bp mRNA linear EST 03-JAN-2002
DEFINITION i960f04.x1 HR85 islet Homo sapiens cDNA 3' similar to SW:STC1_HUMAN
P52823 STANNIOCALCIN 1 PRECURSOR ;, mRNA sequence.
ACCESSION BM311682
VERSION BM311682.1 GI:18046027
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 648)
AUTHORS Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
Lemishka,I., Sgarce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blisstein,A.,
Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas
,M., Gibbons M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T.,
Jackson,Y. and Bowers,Y.
TITLE Endocrine Pancreas Consortium
JOURNAL Unpublished (2000)
COMMENT Other ESTs: i960f04.y1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812

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```

Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Dr. Hiroshi Inoue
(hinoue@im.wustl.edu)
Possible reversed clone: similarity on wrong strand
Seq primer: -40UP from Gibco
High quality sequence stop: 475.

FEATURES
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    /db_xref="taxon:9606"
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    /tissue_type="Purified pancreatic islet"
    /lab_host="DH10B"
    /note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
    NotI; Site_2: XhoI; cDNA made by oligo-dT priming.
    Size-selected on agarose gel. Average insert size ~1kb. 5'
    XhoI site was destroyed after directional cloning.
    Amplified once. Contact information: Hiroshi Inoue, MD,
    Metabolism Div. (Alan Permutt Lab), Washington University
    School of Medicine, Box 8127, 660 South Euclid Ave., St.
    Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
    314-362-1916, Fax: 314-747-2692."
BASE COUNT    175 a 179 c 164 g 130 t
ORIGIN
Alignment Scores:
Pred. No.:      2,18e-197      Length:      648
Score:          207.00         Matches:    207
Percent Similarity: 100.00%     Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match:     83.81%         Indels:    0
DB:              13            Gaps:      0

US-09-705-500A-3 (1-247) x BM311087 (1-648)

QY 13 IleSerAlaSerAlaThrHisGluAlaGluInAsnAspSerValSerProArgLysSer 32
DB 28 ATCAGTGCTTCTGCAACCCATGAGCGGAGCAGATGACTCTGTGAGCCCCAGGAATCC 87
QY 33 ArgValAlaAlaGlnAsnSerAlaGluValAlaArgCysLeuAsnSerAlaLeuGlnVal 52
DB 88 CGAGTGGGGCTCAAACTCAGCTGAGTGGTTCGTGCTCAACAGTCTCTACAGGTC 147
QY 53 GlyCysGlyAlaPheAlaCysLeuGluInAsnSerThrCysAspThrAspMetTyrAsp 72
DB 148 GGCTGGGGGCTTTTGCATGCTCGCTGGAACACTCCACTGTGACACAGATGGGATGTATGAC 207
QY 73 IleCysLysSerPheLeuTyrSerAlaAlaLysPheAspThrGlnGlyLysAlaPheVal 92
DB 208 ATCTGTAAATCTCTTGTACAGCGCTGCTAAATTTGACACTCAGGAAAGCATTCGTC 267
QY 93 LysGlySerLeuLysCysIleAlaAsnGlyValThrSerLysValPheLeuAlaIleArg 112
DB 268 AAAGAGAGCTTAATGATCATCGCAACGGGTCACCTCCAGGCTCTCTCCCATTCGG 327
QY 113 ArgCysSerThrPheGlnArgMetIleAlaGluValGlnGluCysTyrSerLysLeu 132
DB 328 AGGTGCTCCACTTTCCAAAGAGATGATTGCTGAGGTGCGAGGAAGTGTCTACAGCAAGTG 387
QY 133 AsnValCysSerIleAlaLysArgAsnProGluAlaIleThrGluValValGlnLeuPro 152
DB 388 AATGTGTGAGCATTCGCNAGCGGAACCTGGAAGCCATCCTGAGTGTCTCAGCTGCC 447
QY 153 AsnHisPheSerAsnArgTyrTyrAsnArgLeuValArgSerLeuLeuGluCysAspGlu 172
DB 448 AATCACTTCTCCACAGATACATATACAGACTTGTCCGAAGCCTCTGGAATGTATGAA 507
QY 173 AspThrValSerThrIleArgAspSerLeuMetGluLysIleGlyProAsnMetAlaSer 192
DB 508 GACACAGTCAGCAATCAGACAGACGCTGTATGGTGAAGAAATTTGGGCTTAACATGCCAGC 567

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QY 193 LeuPheHisIleLeuGlnThrAspHisCysAlaGlnThrHisProArgAlaAspPheAsn 212
DB 568 CTCCTCCACATCTCTGCAGACAGACCACTGTGCCCAACACACACACAGAGCTGACTTCAAC 627
QY 213 ArgArgArgThrAsnGluPro 219
DB 628 AGGAGACGCACCAATGAGCCG 648

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```

RESULT 4
BM311087/c
LOCUS
DEFINITION
P52823 STANNIOCALCIN 1 PRECURSOR ; mRNA sequence.
ACCESSION
BM311087
VERSION
BM311087.1 GI:18045432
SOURCE
human.

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```

ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 617)
REFERENCE
Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
Lemishka,I., Scarce,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
Hillier,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas
M., Gibbons,M., McCann,R., Cole,R., Teagareishvili,R., Williams,T.,
Jackson,Y. and Bowers,Y.

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KEYWORDS
EST.

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TITLE
Endocrine Pancreas Consortium
JOURNAL
Unpublished (2000)
COMMENT
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Dr. Hiroshi Inoue
(hinoue@im.wustl.edu)

```

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FEATURES
    source
    1..617
    /organism="Homo sapiens"
    /db_xref="taxon:9606"
    /clone_lib="HR85 islet"
    /tissue_type="Purified pancreatic islet"
    /lab_host="DH10B"
    /note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
    NotI; Site_2: XhoI; cDNA made by oligo-dT priming.
    Size-selected on agarose gel. Average insert size ~1kb. 5'
    XhoI site was destroyed after directional cloning.
    Amplified once. Contact information: Hiroshi Inoue, MD,
    Metabolism Div. (Alan Permutt Lab), Washington University
    School of Medicine, Box 8127, 660 South Euclid Ave., St.
    Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
    314-362-1916, Fax: 314-747-2692."
BASE COUNT    123 a 155 c 168 g 171 t
ORIGIN
Alignment Scores:
Pred. No.:      2,1e-195      Length:      617
Score:          205.00         Matches:    205
Percent Similarity: 100.00%     Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match:     83.00%         Indels:    0
DB:              13            Gaps:      0

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US-09-705-500A-3 (1-247) x BM311087 (1-617)

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QY 20 GluAlaGluGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSer 39
 Db 617 GAGGGGAGCAGCAATGACTCTGTGAGCCCGAGAAATCCGAGTGGCGCTCAAAACTCA 558
 QY 40 AlaGluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyValAlaPheAlaCys 59
 Db 557 GCTGAAGTGGTTCGTTGGCTCAACAGTGTCTTACAGGTGGCTGGGGGCTTTTCATGC 498
 QY 60 LeuGluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyr 79
 Db 497 CTGGAAACTCCACTGTGACACAGATGGATGTATGACATCTGTAAATCTTCTTGTAC 438
 QY 80 SerAlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIle 99
 Db 437 AGCGTGTCTAAATTTGACACTCAGGGAAGCATTCGTCAAGAGAGCTTAAATGTCATC 378
 QY 100 AlaAsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArg 119
 Db 377 GCCAACGGGGTCACTCCCAAGGTCTTCTCGCATTCGGAGGTGTCTCCACTTTCCAAAGG 318
 QY 120 MetIleAlaGluValGlnGluCysTyrSerLysLeuAsnValCysSerIleAlaLys 139
 Db 317 ATGATTGTGAGTGCAGGAGAGTGTCTACACAGCTGAATGTGTGAGCATCCCAAG 258
 QY 140 ArgAsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyr 159
 Db 257 CGGAACCCCTGAAGCCACTCACTGAGTGTCTCCAGTGCCTCAATCACTTCTCCAAACAGATAC 198
 QY 160 TyrAsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArg 179
 Db 197 TATACAGACTTGTCCGAAGCCTGTGGAAATGTGATGAAGACACAGTCAACATCAGA 138
 QY 180 AspSerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThr 199
 Db 137 GACACCTGATGGAGAAATTTGGGCTTAACATGGCCGCTTCTTCCATCTCTGGAGACA 78
 QY 200 AspHisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgArgThrAsnGluPro 219
 Db 77 GACCACTGTGCCAAACACACCCAGCTGACTTCAACAGGAGACGACCAATGAGCGC 18
 QY 220 GlnLysLeuLysVal 224
 Db 17 CAGAAGCTGAAAGTC 3

RESULT 5
 LOCUS AW955863 644 bp mRNA linear EST 01-JUN-2000
 DEFINITION EST377936 MAGE resequences, MAGI Homo sapiens cDNA, mRNA sequence.
 ACCESSION AW955863
 VERSION AW955863.1 GI:8155699
 KEYWORDS EST.
 SOURCE human.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 644)
 AUTHORS Hegde, P., Qi, R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C., Holt, I.E., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. and Quackenbush, J.

TITLE Assessment of gene expression patterns in a model of colon tumor metastasis using a 19,200 element cDNA microarray
 JOURNAL Unpublished (2000)
 COMMENT Contact: John Quackenbush
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 3528
 Fax: 301 838 0208
 Email: johnq@tigr.org
 Plate: 220

Seq primer: Reverse.
 Location/Qualifiers
 1. .644

/organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="MAGE resequences, MAGI"
 /note="Vector: pBluescriptSKm"
 BASE COUNT 171 a 175 c 164 g 134 t
 ORIGIN
 Alignment Scores:
 Pred. No.: 2,32e-189 Length: 644
 Score: 199.00 Matches: 199
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 80.57% Indels: 0
 DB: 10 Gaps: 0
 US-09-705-500A-3 (1-247) x AW955863 (1-644)
 QY 5 SerAlaValLeuLeuValLeuValIleSerAlaSerAlaThrHisGluAlaGluGlnAsn 24
 Db 1 TCAGCAGTGTCTTCTGGTGTCTGGTATCAGTGTCTTCAACCCCATGAGCGGAGCAGAA 60
 QY 25 AspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAlaGluValValArg 44
 Db 61 GACTCTGTGAGCCCCAGGAAATCCGAGTGGGGCTCAAACTCAGCTGAAGTGTGTGT 120
 QY 45 CysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeuGluAsnSerThr 64
 Db 121 TGCCTCAACAGTGTCTTACAGTGTGGCTCGGGGCTTTTGCATGCTCGGAAACTCCACC 180
 QY 65 CysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSerAlaAlaLysPhe 84
 Db 181 TGTGACACAGATGGGATGTATGACATCTGTAATTCCTTCTTGTACAGCGCTGCTAAATTT 240
 QY 85 AspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAlaAsnGlyValThr 104
 Db 241 GACACTCAGGGAAGAAAGCATTCGTCAAGAGAGCTTTAAATGCATGCCAACGGGTCCACC 300
 QY 105 SerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMetIleAlaGluVal 124
 Db 301 TCCAAGGTCTTCTCGCCATTCGGAGGTGTCTCCACTTTTCCAAAGGATGATTGCTGAGGTG 360
 QY 125 GlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArgAsnProGluAla 144
 Db 361 CAGGAAGAGTGTCTACAGCAAGTGAATGTGTGACAGCATCGCCACGCGAACTCGAAGCC 420
 QY 145 IleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyrAsnArgLeuVal 164
 Db 421 ATCACTGAGGTGTCTGAGTGTCCAGTGTCCCAATCACTTCTCCAAACAGATCTATAACAGATGGTC 480
 QY 165 ArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAspSerLeuMetGlu 184
 Db 481 CGAAGCCTGTGGAATGTGATGAAGACACAGTCAAGCAATCAGACAGCAGCTGATGGAG 540
 QY 185 LysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAspHisCysAla 203
 Db 541 AAAATTGGGCTTAACATGGCCAGCTCTTCCACATCTCTGCAGACGAGCAATTTGTGCC 597

RESULT 6
 LOCUS AW954342 646 bp mRNA linear EST 01-JUN-2000
 DEFINITION EST366412 MAGE resequences, MAGC Homo sapiens cDNA, mRNA sequence.
 ACCESSION AW954342
 VERSION AW954342.1 GI:8144025
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 646)
 AUTHORS Hegde, P., Qi, R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C., Holt, I.E., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. and Quackenbush, J.

TITLE Assessment of gene expression patterns in a model of colon tumor


```

Db      556 AACGGGGTACCTCAAGGTTCTCTCGCCATTCGAGGTGCTCCACCTTCCAAAGGATG 615
Qy      121 lleAlaGluValGlnGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
Db      616 ATTGCTGAGGTGACGAGAGAGTGTACAGCAAGTGAATGTGTGAGCATCGCCAAAGCG 675
Qy      141 AsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
Db      676 AACCTCTGAAGCATCACTGAGGTGCTCCAGTGCCTCCCAATCACTTCTCCAAACAGATACAT 735
Qy      161 AsnArgLeuValArgSerLeuLeu 168
Db      736 AACAGACTGTCCGAAGCTGTGCTG 759

RESULT 8
AL549427
LOCUS   AL549427 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0D1044Y118 5
DEFINITION
prime, mRNA sequence.
ACCESSION AL549427
VERSION   AL549427.1 GI:12885398
KEYWORDS EST.
SOURCE   human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 782)
Li.W.B., Gruber,C., Jesse,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segre@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
source
1..782
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/sequence="LTI_NFL006_PL2"
/sequence_type="placenta"
/sequence="Vector: pCMVSPORT 6; Site 1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact: Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"

BASE COUNT 230 a 204 c 202 g 144 t 2 others
ORIGIN

Alignment Scores:
Pred. No.: 4.21e-146 Length: 782
Score: 156.00 Matches: 156
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 63.16% Indels: 0
DB: 9 Gaps: 0

US-09-705-500A-3 (1-247) x AL549427 (1-782)

Qy      24. AsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAlaGluValVal 43
Db      313 AATGACTGTGAGCCCGAGAAATCCGAGTGGCGGCTCAAACTCAGCTGAAGTGGTT 372
Qy      44 ArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeuGluAsnSer 63
Db      373 GGTGCTCAACAGTGTCTACAGTTCGGCTCGCGGGCTTTTGCATGCTCGAAACATCC 432

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Qy      64 ThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSerAlaAlaLys 83
Db      433 ACCTGTGCACACAGATGGGATGATGACATCTGTAATCTCTTTGTACAGGCTGCTAAA 492
Qy      84 PheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAlaAsnGlyVal 103
Db      493 TTTGACACTCAGGGAAGAGCATTCGTCAAGAGAGCTTTAAATATGTCATCGCCAAAGGGTC 552
Qy      104 ThrSerLysValPheLeuAlaIleArgCysSerThrPheGlnArgMetIleAlaGlu 123
Db      553 ACCTCCAAAGGTCTTCTCGCCATTCGGAGGTGCTCCACTTTCCAAAGGATGATTCCTGAG 612
Qy      124 ValGlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArgAsnProGlu 143
Db      613 GTGCAGGAAGAGTGTCTACAGCAAGTGAATGTGTGAGCATCGCCAAAGCGAACCCTGAA 672
Qy      144 AlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyrAsnArgLeu 163
Db      673 GCCATCACTGAGGTGCTCCAGTGCCTCCCAATCACTTCTCCAAACAGATACATTAACAGATT 732
Qy      164 ValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArg 179
Db      733 GTCCGAAGCTGCTGGAATGTGATGAAGACACAGTACGACCAATCAGA 780

RESULT 9
BQ308414
LOCUS   BQ308414 MRO-BT4501-280601-103-c11 BT4501 Homo sapiens cDNA, mRNA sequence.
DEFINITION
ACCESSION BQ308414
VERSION   BQ308414.1 GI:20849730
KEYWORDS EST.
SOURCE   human.
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 577)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=MR0&t2=MR0-BT4501-
280601-103-c11&t3=2001-06-28&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 576.
Location/Qualifiers
1..577
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="BT4501"
/dev_stage="Adult"
/note="Organ: breast; Vector: puc18; Site:1: SmaI; Site:2:
SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No. 196
716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."

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BASE COUNT      161 a   159 c   140 g   117 t
ORIGIN

Alignment Scores:
Pred. No.:      3,55e-125      Length:      577
Score:          135.00         Matches:      148
Percent Similarity: 99.33%      Conservative: 0
Best Local Similarity: 99.33%      Mismatches: 0
Query Match:      54.66%      Indels:      1
DB:              14           Gaps:         0

US-09-705-500A-3 (1-247) x BQ308414 (1-577)
QY 68 AspGlyMetTyrAspIleCysLysSerPheLeuTyrSerAlaAlaLysPheAspThrGln 87
DB 89 GATGGAGTATGACATCTGTAATCTTCTGTACAGCGCTGCTAAATTTGACACTCAG 148
QY 88 GlyLysAlaPheValLysGluSerLeuLysCysIleAlaAsnGlyValThrSerLysVal 107
DB 149 CGAAAGGCAATTCCTCAAGAGAGCTTAAATGCATCGCCACCGGGTCACTCCCAAGGTC 208
QY 108 PheLeuAlaIleArgArgSerThrPheGlnArgMetIleAlaGluValGlnGluGlu 127
DB 209 TTCCTCGCCATTCGAGAGGCTCCACTTTCCAAAGGATGATTGCTGAGGTGCGAGAGAG 268
QY 128 CysTyrSerLysLeuAsnValCysSerIleAlaLysArgAsnProGluAlaIleThrGlu 147
DB 269 TGTACACAGCTGAATGTGTGAGCATCGCAGCGGACCTGAGCCATCACTCAG 328
QY 148 ValValGlnLeuProAsnHisPheSerAsnArgTyrTyrAsnArgLeuValArgSerLeu 167
DB 329 GTGCTCCAGCTGCCCAATCACTTCTCCACAGATACTATAACAGACTTGTCCGAAGCCTG 388
QY 168 LeuGluCysAspGluAspThrValSerThrIleArgAspSerLeuMetGluLysIleGly 187
DB 389 CTGGAATGTGATGAAGACACAGTCAGCACAATCAGACAGACGCTGATGGAGAAATGGG 448
QY 188 ProAsnMetAlaSerLeuPheHisIleLeuGlnThrAspHisCysAlaGlnThrHisPr 207
DB 449 CCTAAACATGGCCAGCCTTCCATCATCTGAGACAGACCACTGTGCGCCAAACACACC 508
QY 207 QArgAlaAspPheAsnArgArgArg 215
DB 509 ACGAGTGAATTCACAGAGAGAGC 533

RESULT 10
AUI22680      907 bp      mRNA      linear      EST 01-AUG-2002
LOCUS      AUI22680 MAMMA1 Homo sapiens cDNA clone MAMMA1002879 5', mRNA
DEFINITION      sequence.
ACCESSION      AUI22680
VERSION      AUI22680.1 GI:10947396
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 907)
AUTHORS      Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saiko,K., Kawai,Y.,
Yanamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
Isogai,T.
TITLE      HRI human cDNA project
JOURNAL      Unpublished (2000)
COMMENT      Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and

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FEATURES
    source          Helix Research Institute.
    Location/Qualifiers
        1..907
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            /clone="MAMMA1002879"
            /clone_lib="MAMMA1"
            /tissue_type="mammary gland"
            /note="Vector: pME18SFL3"
BASE COUNT      264 a   230 c   229 g   178 t
ORIGIN

Alignment Scores:
Pred. No.:      6.72e-112      Length:      907
Score:          122.00         Matches:      122
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:      49.39%      Indels:      0
DB:              9           Gaps:         0

US-09-705-500A-3 (1-247) x AUI22680 (1-907)
QY 1 MetLeuGlnAsnSerAlaValLeuValLeuValLeuValLeuValLeuValLeuValLeuVal 20
DB 283 ATGCTCCAAAACCTCAGCGGTCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 342
QY 21 AlaGluGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
DB 343 CGGAGCAGAAATGACTCTGTGAGCCCGAGAAATCCCGAGTGGCGGCTCAAACTCAGCT 402
QY 41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
DB 403 GAAGTGGTGTCTTCCCTCAACAGTGTCTACAGTTCGGCTCGGGGCTTTTTCATGCTG 462
QY 61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
DB 463 GAAACATCCACCTGACACAGATGGGATGTATGACATCTGTAAATCCTTCTGTGTACAGC 522
QY 81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAla 100
DB 523 GCTGCTAAATTTGACATCAGGGAAGAAGCATCTGTCAAAGAGAGCTTAAATGATGCC 582
QY 101 AsnGlyValThrSerLysValPheLeuAlaIleArgCysSerThrPheGlnArgMet 120
DB 583 AACGGGTGTCACCTCAAGGTCTTCTCGCCATTCGGAGTGTCTCCACTTCCCAAGGATG 642
QY 121 IleAla 122
DB 643 ATTGCT 648

RESULT 11
BM924595      1010 bp      mRNA      linear      EST 12-MAR-2002
LOCUS      AGENCOURT 6767843 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5760977
DEFINITION      5', mRNA sequence.
ACCESSION      BM924595
VERSION      BM924595.1 GI:19374974
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 1010)
AUTHORS      NIH-MGC http://mgs.nci.nih.gov/
TITLE      National Institutes of Health
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be

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BI010412
LOCUS       BI010412               605 bp    mRNA    linear    EST 13-JUN-2001
DEFINITION MR2-EN0094-050101-007-d02 EN0094 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BI010412
VERSION     BI010412.1   GI:14414483
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 605)
AUTHORS     Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
             Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
             Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
             Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
             M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
             Simpson,A.J.
TITLE       Shotgun sequencing of the human transcriptome with ORF expressed
             sequence tags
JOURNAL     Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE     20202663
COMMENT     Contact: Simpson A.J.G.
             Laboratory of Cancer Genetics
             Ludwig Institute for Cancer Research
             Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
             Brazil
             Tel: +55-11-2704922
             Fax: +55-11-2707001
             Email: asimpson@ludwig.org.br
             This sequence was derived from the FAPESP/LICR Human Cancer Genome
             Project. This entry can be seen in the following URL
             (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=MR2&t2=MR2-EN0094-
             050101-007-d02&t3=2001-01-05&t4=1)
             Seq primer: puc 18 forward
             High quality sequence stop: 605.
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                 /dev_stage="Adult"
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                 Site_2: SmaI; A mini-library was made by cloning products
                 derived from ORESTES PCR (U.S. Letters Patent application
                 No. 196,716 - Ludwig Institute for Cancer Research)
                 profiles into the pUC 18 vector. Reverse transcription of
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                 low stringency conditions."
BASE COUNT  173 a 174 c 117 g 140 t
ORIGIN
Alignment Scores:
Pred. No.:      4,94e-93      Length:      605
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DB:             13          Gaps:        0

US-09-705-500A-3 (1-247) x BI010412 (1-605)

Qy      145  lleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyrAsnArgLeuVal 164
Db      24  ATCACTGAGGTGCTCCAGTGCCTCAATCACTTCTCCACAGACTATATAACAGACTTGTC 83

Qy      165  ArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAspSerLeuWetGlu 184
Db      84  CGAAGCCTGCTGGAATGTGATGAAGACAGTCAGCAATCAGACAGCGCTGATGAG 143

Qy      185  LysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAspHisCysAlaGln 204
Db      144  AAANITGGCCCTAACATGGCCAGCCTCTTCCACATCTTCGACAGACAGCACTGTGCCCAA 203

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Qy      205  ThrHisProArgAlaAspPheAsnArgArgThrAsnGluProGlnLysLeuLysVal 224
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Qy      225  LeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHisIleLeuYsArgThrSerHis 244
Db      264  CTCCTCAGGAACCTCCGAGGTGAGGAGGACTCTCCCTCCACATCAAAACGACATCCCAT 323

Qy      245  GluSerAla 247
Db      324  GAGAGTGCA 332

RESULT 14
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LOCUS     R72337
DEFINITION Y189d08.rl Soares breast 2NbHBst Homo sapiens cDNA clone
IMAGE:155919 5', similar to SP:CSFP_ANGAU P18301 CORPUSCLES OF
STANNIUS PROTEIN PRECURSOR ;, mRNA sequence.
ACCESSION R72337
VERSION   R72337.1   GI:846369
KEYWORDS  EST.
SOURCE    human.
ORGANISM  Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 483)
AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman
             M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J.,
             Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston
             R., Williamson,A., Wohlmann,P. and Wilson,R.
             The WashU-Merck EST Project
             Unpublished (1995)
             Contact: Wilson RK
             Washington University School of Medicine
             4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
             Tel: 314 286 1800
             Fax: 314 286 1810
             Email: est@watson.wustl.edu
             Insert Size: 1711
             High quality sequence stops: 355
             Source: IMAGE Consortium, LLNL
             This clone is available royalty-free through LLNL ; contact the
             IMAGE Consortium (info@image.llnl.gov) for further information.
             Insert Length: 1711 Std Error: 0.00
             Seq primer: M13Rp1
             High quality sequence stop: 355.
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                 /clone="IMAGE:155919"
                 /clone_lib="Soares breast 2NbHBst"
                 /sex="Female"
                 /dev_stage="adult"
                 /lab_host="DH10B (ampicillin resistant)"
                 /note="Organ: breast; Vector: pT7T3D (Pharmacia) with a
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                 strand cDNA was primed with a Not I - oligo(dT) primer [5',
                 TGTTACCAATCTGAAGTGGAGCGCGCCCTTTTCTTTTCTTTT 3'],
                 double-stranded cDNA was ligated to Eco RI adaptors
                 (Pharmacia), digested with Not I and cloned into the Not I
                 and Eco RI sites of a modified pT7T3 vector (Pharmacia).
                 Library went through one round of normalization to a Cot =
                 230. Library constructed by Bento Soares and M.Fatima
                 Bonaldo."
BASE COUNT  135 a 127 c 119 g 97 t 5 others
ORIGIN
Alignment Scores:
Pred. No.:      3,94e-89      Length:      483
Score:          99.00      Matches:     125
Percent Similarity: 98.43%      Conservative: 0

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Best Local Similarity: 98.43% Mismatches: 0
Query Match: 40.08% Indels: 2
DB: 14 Gaps: 0

US-09-705-500A-3 (1-247) x R72337 (1-483)

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Dy 3 AAAGCATTCGTCAAGAGAGCTTAAATGATCGCAACGGGGTCACTCCAAAGTCTTC 62
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Dy 63 CTCGCCATTCGAGGTCTCCACTTTCAAAGATGATGCTGAGTGCAGGAAGTGC 122
Qy 129 TyrSerLysLeuAsnValCysSerIleAlaLysArgAsnProGluAlaIleThrGluVal 148
Dy 123 TACAGCAAGCTCAATGTGTGAGCATCGCAAGCGAACCTTGAAGCCATCACTGAGTGC 182
Qy 149 ValGlnLeuProAsnHisPheSerAsnArgTyrTyrAsnArgLeuValArgSerLeuLeu 168
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Dy 243 GAATGTGATGAGACACAGCTGACCAATCAGACAGCCCTGATGGGAAATTTGGGC 302
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Dy 303 CTAACATGCCAGCTCTTCCACATCTCTGCACAGACAGCCACTGTGCCCAACACACACCAC 362
Qy 208 tGAlaAspPheAsnArg 213
Dy 363 GAGCTGACTTCAACAGG 379

RESULT 15
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DEFINITION QV3-BN0046-150400-151-b06 BN0046 Homo sapiens cDNA, mRNA sequence.
ACCESSION AW996662
VERSION AW996662.1 GI:8256896
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 437)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W.Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
2020663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl1=&t2=QV3-BN0046-150
400-151-b06&t3=2000-04-15&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 41
High quality sequence stop: 437.
Location/Qualifiers
1. .437

TITLE
JOURNAL
MEDLINE
COMMENT

FEATURES
source

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="BN0046"
/dev_stage="Adult"

/note="Organ: breast normal; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

BASE COUNT 75 a 102 c 130 g 130 t
ORIGIN

Alignment Scores:
Pred. No.: 3.63e-85 Length: 437
Score: 95.00 Matches: 130
Percent Similarity: 98.48% Conservative: 0
Best Local Similarity: 98.48% Mismatches: 1
Query Match: 38.46% Indels: 2
DB: 10 Gaps: 0

US-09-705-500A-3 (1-247) x AW996662 (1-437)

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Dy 435 ACTTTCCAAAGGATGATTGCTGAGGTGCAGGAAGTGTCTACAGCAAGCTGAATGTGTGC 376
Qy 136 SerIleAlaLysArgAsnProGluAlaIleThrGluValValGlnLeuProAsnHisPhe 155
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Qy 156 SerAsnArgTyrTyrAsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrVal 175
Dy 315 TCCAAACAGATATAACAGACTTGTCCGAAGCCTGCTGGAATGTGATGAAGACACAGTC 256
Qy 176 SerThrIleArgAspSerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHis 195
Dy 255 AGCAATATCAGAGACAGCCTGATGGAGAAAATTGGGCTTAACATGGCCAGGCTCTTCCAC 196
Qy 196 IleLeuGlnThrAspHisCysAlaGlnThrHisProArgAlaAspPhe-AsnArgArgAr 215
Dy 195 ATCTCGACAGACAGACCCTGTGCCCAACACACCCACGAGCTGAGCT-CAACAGGAGAGC 137
Qy 215 gThrAsnGluProGlnLysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSe 235
Dy 136 CACCAATGAGCCGAGAGGCTGAAGTCTCTCTCAGGAACCTCCGAGGTGAGGAGGACTC 77
Qy 235 rProSerHisIleLysArgThrSerHisGluSer 246
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Search completed: June 12, 2003, 23:07:38
Job time : 1487 secs

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c 103	38	1.0	87	3	US-08-481-710-74	Sequence 74, Appl	c 176	38	1.0	97	4	US-08-952-793-390	Sequence 390, App
c 104	38	1.0	87	3	US-08-481-710-186	Sequence 186, App	c 177	38	1.0	97	5	PCT-US96-09455A-248	Sequence 248, App
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c 108	38	1.0	87	3	US-08-793-398-4	Sequence 4, Appl	c 181	38	1.0	104	1	US-08-591-989-11	Sequence 11, Appl
c 109	38	1.0	87	3	US-08-793-398-4	Sequence 4, Appl	c 182	38	1.0	104	1	US-08-591-989-11	Sequence 11, Appl
c 110	38	1.0	87	3	US-08-793-965-13	Sequence 13, Appl	c 183	38	1.0	104	2	US-08-139-176D-2	Sequence 2, Appl
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c 132	38	1.0	87	5	PCT-US96-09472-64	Sequence 64, Appl	c 205	38	1.0	147	2	US-08-618-700-6	Sequence 6, Appl
c 133	38	1.0	87	5	PCT-US96-08014-49	Sequence 49, Appl	c 206	38	1.0	147	2	US-08-618-700-6	Sequence 6, Appl
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c 135	38	1.0	87	5	PCT-US96-08014-52	Sequence 52, Appl	c 208	38	1.0	147	2	US-08-618-700-7	Sequence 7, Appl
c 136	38	1.0	87	5	PCT-US96-08014-52	Sequence 52, Appl	c 209	38	1.0	147	2	US-08-618-700-7	Sequence 7, Appl
c 137	38	1.0	87	5	PCT-US96-09472-64	Sequence 64, Appl	c 210	38	1.0	147	3	US-09-157-601-6	Sequence 6, Appl
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c 157	38	1.0	96	1	US-08-479-783A-36	Sequence 36, Appl	c 230	38	1.0	608	5	PCT-US96-02331-11	Sequence 11, Appl
c 158	38	1.0	96	1	US-08-479-783A-36	Sequence 36, Appl	c 231	38	1.0	750	4	US-08-821-994-40	Sequence 40, Appl
c 159	38	1.0	96	1	US-08-479-725-36	Sequence 36, Appl	c 232	38	1.0	959	4	US-09-724-510-1	Sequence 1, Appl
c 160	38	1.0	96	1	US-08-479-725-36	Sequence 36, Appl	c 233	38	1.0	959	4	US-09-723-216-1	Sequence 1, Appl
c 161	38	1.0	96	1	US-08-618-693-36	Sequence 36, Appl	c 234	38	1.0	959	4	US-09-675-227-1	Sequence 1, Appl
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c 163	38	1.0	96	4	US-08-973-124-125	Sequence 125, App	c 236	38	1.0	1070	4	US-09-718-841-3	Sequence 3, Appl
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c 165	38	1.0	96	4	US-08-991-743C-36	Sequence 36, Appl	c 238	38	1.0	1280	4	US-09-276-531-52	Sequence 52, Appl
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c 169	38	1.0	97	1	US-08-447-172A-1	Sequence 1, Appl	c 242	38	1.0	1738	4	US-09-515-039-89	Sequence 89, Appl
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c 171	38	1.0	97	1	US-08-447-172A-4	Sequence 4, Appl	c 244	38	1.0	4997	1	US-08-232-463-1	Sequence 1, Appl
c 172	38	1.0	97	1	US-08-447-172A-4	Sequence 4, Appl	c 245	38	1.0	8285	4	US-09-732-025-3	Sequence 3, Appl
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248	38	1.0	9454	1	US-08-232-463-3	Sequence 3, Appli	321	37	1.0	71	2	US-08-465-591A-1	Sequence 1, Appli
249	38	1.0	9454	1	US-08-232-463-4	Sequence 4, Appli	322	37	1.0	71	2	US-08-465-591A-1	Sequence 1, Appli
250	38	1.0	11528	3	US-08-444-644-18	Sequence 18, Appli	323	37	1.0	71	2	US-08-465-594A-1	Sequence 1, Appli
251	38	1.0	11528	4	US-08-232-246A-18	Sequence 18, Appli	324	37	1.0	71	2	US-08-465-594A-1	Sequence 1, Appli
252	38	1.0	11827	4	US-09-739-455-3	Sequence 3, Appli	325	37	1.0	71	2	US-08-484-522A-33	Sequence 33, Appli
253	38	1.0	19806	4	US-09-740-028A-3	Sequence 3, Appli	326	37	1.0	71	2	US-08-484-522A-33	Sequence 33, Appli
254	38	1.0	38564	4	US-09-734-673-3	Sequence 3, Appli	327	37	1.0	71	2	US-08-460-888A-38	Sequence 38, Appli
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258	37	1.0	39	2	US-08-659-453B-2	Sequence 2, Appli	331	37	1.0	71	2	US-08-477-527A-256	Sequence 256, Appli
259	37	1.0	39	3	US-09-089-853A-2	Sequence 2, Appli	332	37	1.0	71	2	US-08-477-527A-256	Sequence 256, Appli
260	37	1.0	39	4	US-09-131-009A-2	Sequence 2, Appli	333	37	1.0	71	2	US-08-894-578-38	Sequence 38, Appli
261	37	1.0	39	4	US-09-092-226A-2	Sequence 2, Appli	334	37	1.0	71	2	US-08-894-578-38	Sequence 38, Appli
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263	37	1.0	39	4	US-09-090-809A-2	Sequence 2, Appli	336	37	1.0	71	3	US-08-472-256B-64	Sequence 64, Appli
264	37	1.0	39	4	US-09-053-116A-2	Sequence 2, Appli	337	37	1.0	71	3	US-08-481-710-1	Sequence 1, Appli
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266	37	1.0	44	3	US-09-089-853A-22	Sequence 22, Appli	339	37	1.0	71	3	US-08-481-710-256	Sequence 256, Appli
267	37	1.0	44	4	US-09-131-009A-22	Sequence 22, Appli	340	37	1.0	71	3	US-08-481-710-256	Sequence 256, Appli
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269	37	1.0	44	4	US-09-130-862A-22	Sequence 22, Appli	342	37	1.0	71	3	US-09-046-247-1	Sequence 1, Appli
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275	37	1.0	62	4	US-09-131-009A-4	Sequence 4, Appli	348	37	1.0	71	4	US-08-973-124-46	Sequence 46, Appli
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395	37	1.0	72	3	US-08-976-413A-1	Sequence 1, Appli	468	37	1.0	110	4	US-08-299-498A-3	Sequence 3, Appli
396	37	1.0	72	3	US-08-976-413A-1	Sequence 1, Appli	469	37	1.0	110	5	PCT-US95-10813-3	Sequence 3, Appli
397	37	1.0	72	5	PCT-US96-06039-1	Sequence 1, Appli	470	37	1.0	112	1	US-08-299-498A-32	Sequence 32, Appli
398	37	1.0	72	5	PCT-US96-06039-1	Sequence 1, Appli	471	37	1.0	112	5	PCT-US95-10813-32	Sequence 32, Appli
399	37	1.0	72	5	PCT-US96-09472-1	Sequence 1, Appli	c 472	37	1.0	120	1	US-07-843-125-4	Sequence 4, Appli
400	37	1.0	72	5	PCT-US96-09472-1	Sequence 1, Appli	473	37	1.0	120	2	US-08-787-042-1	Sequence 1, Appli
401	37	1.0	74	1	US-09-193-068-15	Sequence 15, Appli	c 474	37	1.0	120	2	US-08-787-042-1	Sequence 1, Appli
402	37	1.0	75	1	US-08-437-815-10	Sequence 10, Appli	c 475	37	1.0	121	4	US-09-535-754-10	Sequence 10, Appli
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405	37	1.0	78	4	US-09-193-068-17	Sequence 17, Appli	478	37	1.0	134	5	PCT-US95-10813-5	Sequence 5, Appli
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408	37	1.0	80	1	US-08-472-194A-4	Sequence 4, Appli	c 481	37	1.0	154	4	US-09-407-715-7	Sequence 7, Appli
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410	37	1.0	80	4	US-08-849-567A-4	Sequence 4, Appli	c 483	37	1.0	195	4	US-08-842-445-64	Sequence 64, Appli
411	37	1.0	81	1	US-08-399-412A-4	Sequence 4, Appli	c 484	37	1.0	195	4	US-09-186-188B-64	Sequence 64, Appli
412	37	1.0	81	1	US-08-399-412A-4	Sequence 4, Appli	c 485	37	1.0	207	2	US-08-039-198B-6	Sequence 6, Appli
413	37	1.0	81	1	US-08-384-708A-98	Sequence 98, Appli	c 486	37	1.0	212	4	US-09-574-141A-86	Sequence 86, Appli
414	37	1.0	81	1	US-08-384-708A-98	Sequence 98, Appli	c 487	37	1.0	215	4	US-09-535-754-8	Sequence 8, Appli
415	37	1.0	81	1	US-08-447-169A-60	Sequence 60, Appli	c 488	37	1.0	231	4	US-08-679-453A-13	Sequence 13, Appli
416	37	1.0	81	1	US-08-447-169A-60	Sequence 60, Appli	489	37	1.0	313	4	US-09-094-381C-1	Sequence 1, Appli
417	37	1.0	81	2	US-08-233-012C-60	Sequence 60, Appli	490	37	1.0	313	4	US-09-094-381C-2	Sequence 2, Appli
418	37	1.0	81	2	US-08-233-012C-60	Sequence 60, Appli	491	37	1.0	313	4	US-09-094-381C-3	Sequence 3, Appli
419	37	1.0	81	3	US-09-023-228B-2	Sequence 2, Appli	492	37	1.0	313	4	US-09-094-381C-4	Sequence 4, Appli
420	37	1.0	81	3	US-09-023-228B-2	Sequence 2, Appli	493	37	1.0	313	4	US-09-094-381C-5	Sequence 5, Appli
421	37	1.0	81	4	US-08-687-421-98	Sequence 98, Appli	494	37	1.0	321	4	US-09-094-381C-25	Sequence 25, Appli
422	37	1.0	81	4	US-08-687-421-98	Sequence 98, Appli	495	37	1.0	321	4	US-09-094-381C-26	Sequence 26, Appli
423	37	1.0	81	4	US-09-193-068-19	Sequence 19, Appli	496	37	1.0	321	4	US-09-094-381C-27	Sequence 27, Appli
424	37	1.0	81	4	US-09-163-025B-157	Sequence 157, Appli	497	37	1.0	321	4	US-09-094-381C-28	Sequence 28, Appli
425	37	1.0	81	4	US-09-163-025B-157	Sequence 157, Appli	498	37	1.0	321	4	US-09-094-381C-29	Sequence 29, Appli
426	37	1.0	83	4	US-08-687-421-325	Sequence 325, Appli	c 499	37	1.0	324	2	US-08-378-939-21	Sequence 21, Appli
427	37	1.0	86	1	US-07-964-624D-43	Sequence 43, Appli	500	37	1.0	324	2	US-08-378-939-21	Sequence 21, Appli
428	37	1.0	86	1	US-08-442-062-43	Sequence 43, Appli	501	37	1.0	345	4	US-09-025-203-16	Sequence 16, Appli
429	37	1.0	86	1	US-08-748-697A-43	Sequence 43, Appli	502	37	1.0	495	2	US-08-465-380-31	Sequence 31, Appli
430	37	1.0	86	4	US-09-165-616-43	Sequence 43, Appli	503	37	1.0	495	2	US-08-486-397-31	Sequence 31, Appli
431	37	1.0	88	4	US-08-870-930-2	Sequence 2, Appli	504	37	1.0	495	2	US-08-486-399-31	Sequence 31, Appli
432	37	1.0	88	4	US-08-870-930-2	Sequence 2, Appli	505	37	1.0	495	2	US-08-461-965-31	Sequence 31, Appli
433	37	1.0	88	4	US-09-364-539-15	Sequence 15, Appli	c 506	37	1.0	551	2	US-08-647-368A-4	Sequence 4, Appli
434	37	1.0	88	4	US-09-364-539-15	Sequence 15, Appli	507	37	1.0	605	3	US-09-109-204-19	Sequence 19, Appli
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436	37	1.0	88	4	US-09-363-939A-4	Sequence 4, Appli	509	37	1.0	633	4	US-09-812-484-25	Sequence 25, Appli
437	37	1.0	88	4	US-09-254-968-134	Sequence 134, Appli	510	37	1.0	738	1	US-07-843-125-2	Sequence 2, Appli
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439	37	1.0	90	4	US-08-679-493A-17	Sequence 17, Appli	c 512	37	1.0	759	3	US-09-103-205-11	Sequence 11, Appli
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449	37	1.0	98	1	US-08-234-613-4	Sequence 4, Appli	c 522	37	1.0	1183	2	US-08-731-722-8	Sequence 8, Appli
450	37	1.0	98	1	US-08-399-412A-7	Sequence 7, Appli	523	37	1.0	1285	2	US-08-039-198B-7	Sequence 7, Appli
451	37	1.0	98	1	US-08-447-172A-28	Sequence 28, Appli	524	37	1.0	1457	2	US-08-039-198B-1	Sequence 1, Appli
452	37	1.0	98	1	US-08-447-172A-31	Sequence 31, Appli	c 525	37	1.0	1457	2	US-08-039-198B-1	Sequence 1, Appli
453	37	1.0	98	1	US-08-472-255A-1	Sequence 1, Appli	526	37	1.0	1471	2	US-08-039-198B-8	Sequence 8, Appli
454	37	1.0	98	1	US-08-479-724A-1	Sequence 4, Appli	c 527	37	1.0	1471	2	US-08-039-198B-8	Sequence 8, Appli
455	37	1.0	98	2	US-08-237-973-4	Sequence 4, Appli	528	37	1.0	1471	2	US-08-039-198B-8	Sequence 8, Appli
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459	37	1.0	98	4	US-08-952-793-1	Sequence 1, Appli	c 532	37	1.0	1713	4	US-08-759-436-1	Sequence 1, Appli
460	37	1.0	98	4	US-08-849-567A-50	Sequence 50, Appli	c 533	37	1.0	1750	3	US-09-120-365-90	Sequence 90, Appli
461	37	1.0	98	4	US-09-163-025B-156	Sequence 156, Appli	534	37	1.0	1750	4	US-09-515-039-90	Sequence 90, Appli
462	37	1.0	98	4	US-09-163-025B-156	Sequence 156, Appli	535	37	1.0	1769	4	US-09-484-970B-46	Sequence 46, Appli
463	37	1.0	98	5	PCT-US96-09455A-1	Sequence 1, Appli	c 536	37	1.0	1769	4	US-09-484-970B-46	Sequence 46, Appli
464	37	1.0	99	4	US-08-679-493A-18	Sequence 18, Appli	c 537	37	1.0	1782	1	US-08-374-155A-13	Sequence 13, Appli
465	37	1.0	99	4	US-08-849-567A-51	Sequence 51, Appli	c 538	37	1.0	1782	2	US-08-785-396-13	Sequence 13, Appli
										2030	4	US-09-484-970B-152	Sequence 152, Appli

C 539	37	1.0	2038	4	US-09-276-531-37	Sequence 37, Appl	612	36	1.0	39	4	US-09-090-809A-2	Sequence 2, Appl
C 540	37	1.0	2087	4	US-09-484-970B-153	Sequence 153, App	613	36	1.0	39	4	US-09-053-116A-2	Sequence 2, Appl
C 541	37	1.0	2116	2	US-08-663-566A-18	Sequence 18, Appl	614	36	1.0	40	3	US-09-028-128A-1	Sequence 1, Appl
C 542	37	1.0	2116	2	US-08-023-610-18	Sequence 18, Appl	615	36	1.0	40	3	US-09-028-128A-1	Sequence 1, Appl
C 543	37	1.0	2116	2	US-08-288-065A-18	Sequence 18, Appl	616	36	1.0	42	2	US-08-659-453B-14	Sequence 14, Appl
C 544	37	1.0	2116	2	US-08-362-240A-18	Sequence 18, Appl	617	36	1.0	42	2	US-08-659-453B-14	Sequence 14, Appl
C 545	37	1.0	2116	5	PCT-US95-10245-18	Sequence 18, Appl	618	36	1.0	42	3	US-09-089-853A-14	Sequence 14, Appl
C 546	37	1.0	2215	3	US-08-891-789B-7	Sequence 7, Appl	619	36	1.0	42	3	US-09-089-853A-14	Sequence 14, Appl
C 547	37	1.0	2215	3	US-08-891-789B-7	Sequence 7, Appl	620	36	1.0	42	3	US-09-131-009A-14	Sequence 14, Appl
C 548	37	1.0	2428	2	US-08-849-536A-3	Sequence 3, Appl	621	36	1.0	42	4	US-09-131-009A-14	Sequence 14, Appl
C 549	37	1.0	2793	1	US-08-209-747-1	Sequence 1, Appl	622	36	1.0	42	4	US-09-092-226A-14	Sequence 14, Appl
C 550	37	1.0	2793	1	US-08-458-298-1	Sequence 1, Appl	623	36	1.0	42	4	US-09-092-226A-14	Sequence 14, Appl
C 551	37	1.0	2847	4	US-09-484-970B-22	Sequence 22, Appl	624	36	1.0	42	4	US-09-130-862A-14	Sequence 14, Appl
C 552	37	1.0	3141	2	US-08-956-242-1	Sequence 1, Appl	625	36	1.0	42	4	US-09-130-862A-14	Sequence 14, Appl
C 553	37	1.0	3141	2	US-08-956-242-1	Sequence 1, Appl	626	36	1.0	42	4	US-09-090-809A-14	Sequence 14, Appl
C 554	37	1.0	3141	3	US-09-351-215-1	Sequence 1, Appl	627	36	1.0	42	4	US-09-090-809A-14	Sequence 14, Appl
C 555	37	1.0	3141	3	US-09-351-215-1	Sequence 1, Appl	628	36	1.0	42	4	US-09-053-116A-14	Sequence 14, Appl
C 556	37	1.0	3846	2	US-08-845-161A-5	Sequence 5, Appl	629	36	1.0	42	4	US-09-053-116A-14	Sequence 14, Appl
C 557	37	1.0	3846	2	US-08-845-161A-5	Sequence 5, Appl	630	36	1.0	42	4	US-08-659-453B-22	Sequence 22, Appl
C 558	37	1.0	3846	4	US-09-270-751-5	Sequence 5, Appl	631	36	1.0	44	2	US-09-089-853A-22	Sequence 22, Appl
C 559	37	1.0	3846	4	US-09-270-751-5	Sequence 5, Appl	632	36	1.0	44	4	US-09-131-009A-22	Sequence 22, Appl
C 560	37	1.0	3846	4	US-09-168-218B-3	Sequence 3, Appl	633	36	1.0	44	4	US-09-092-226A-22	Sequence 22, Appl
C 561	37	1.0	3846	4	US-09-168-218B-3	Sequence 3, Appl	634	36	1.0	44	4	US-09-130-862A-22	Sequence 22, Appl
C 562	37	1.0	4339	4	US-09-484-970B-164	Sequence 164, App	635	36	1.0	44	4	US-09-090-809A-22	Sequence 22, Appl
C 563	37	1.0	4701	3	US-08-651-472-64	Sequence 64, Appl	636	36	1.0	44	4	US-09-053-116A-22	Sequence 22, Appl
C 564	37	1.0	4701	4	US-08-358-928-64	Sequence 64, Appl	637	36	1.0	57	2	US-08-136-214-8	Sequence 8, Appl
C 565	37	1.0	4772	4	US-09-484-970B-133	Sequence 133, App	638	36	1.0	57	2	US-08-136-214-8	Sequence 8, Appl
C 566	37	1.0	4858	4	US-09-392-184-1	Sequence 1, Appl	639	36	1.0	66	1	US-08-748-697A-13	Sequence 13, Appl
C 567	37	1.0	6775	4	US-09-402-929-4	Sequence 4, Appl	640	36	1.0	66	1	US-08-748-697A-13	Sequence 13, Appl
C 568	37	1.0	8285	4	US-09-732-025-3	Sequence 3, Appl	641	36	1.0	66	4	US-08-952-793-292	Sequence 292, App
C 569	37	1.0	8299	1	US-08-462-014-2	Sequence 2, Appl	642	36	1.0	66	4	US-08-952-793-292	Sequence 292, App
C 570	37	1.0	8299	3	US-08-923-137-3	Sequence 3, Appl	643	36	1.0	66	4	US-09-165-616-13	Sequence 13, Appl
C 571	37	1.0	8299	4	US-08-973-334-5	Sequence 5, Appl	644	36	1.0	66	4	US-09-165-616-13	Sequence 13, Appl
C 572	37	1.0	8299	4	US-09-563-869A-5	Sequence 5, Appl	645	36	1.0	66	5	PCT-US96-09455A-292	Sequence 292, App
C 573	37	1.0	10785	3	US-08-444-644-27	Sequence 27, Appl	646	36	1.0	66	5	PCT-US96-09455A-292	Sequence 292, App
C 574	37	1.0	10785	3	US-08-444-644-27	Sequence 27, Appl	647	36	1.0	67	1	US-08-260-582-3	Sequence 3, Appl
C 575	37	1.0	10785	4	US-08-232-246A-27	Sequence 27, Appl	648	36	1.0	67	3	US-07-876-288-14	Sequence 14, Appl
C 576	37	1.0	10785	4	US-08-232-246A-27	Sequence 27, Appl	649	36	1.0	67	5	PCT-US95-05471-3	Sequence 3, Appl
C 577	37	1.0	10844	3	US-08-444-644-41	Sequence 41, Appl	650	36	1.0	68	2	US-08-659-453B-9	Sequence 9, Appl
C 578	37	1.0	10844	3	US-08-444-644-41	Sequence 41, Appl	651	36	1.0	68	3	US-09-089-853A-9	Sequence 9, Appl
C 579	37	1.0	10844	3	US-08-232-246A-41	Sequence 41, Appl	652	36	1.0	68	4	US-09-131-009A-9	Sequence 9, Appl
C 580	37	1.0	10844	4	US-08-232-246A-41	Sequence 41, Appl	653	36	1.0	68	4	US-09-092-226A-9	Sequence 9, Appl
C 581	37	1.0	11827	4	US-09-739-455-3	Sequence 3, Appl	654	36	1.0	68	4	US-09-130-862A-9	Sequence 9, Appl
C 582	37	1.0	12127	3	US-08-444-644-32	Sequence 32, Appl	655	36	1.0	68	4	US-09-090-809A-9	Sequence 9, Appl
C 583	37	1.0	12127	3	US-08-444-644-32	Sequence 32, Appl	656	36	1.0	68	4	US-09-053-116A-9	Sequence 9, Appl
C 584	37	1.0	12127	3	US-08-232-246A-32	Sequence 32, Appl	657	36	1.0	71	1	US-08-458-423A-5	Sequence 5, Appl
C 585	37	1.0	12127	4	US-08-232-246A-32	Sequence 32, Appl	658	36	1.0	71	1	US-08-458-423A-5	Sequence 5, Appl
C 586	37	1.0	12127	4	US-08-390-878-18	Sequence 18, Appl	659	36	1.0	71	1	US-08-458-424B-5	Sequence 5, Appl
C 587	37	1.0	13877	4	US-09-484-970B-60	Sequence 60, Appl	660	36	1.0	71	1	US-08-458-424B-5	Sequence 5, Appl
C 588	37	1.0	13999	3	US-08-444-644-24	Sequence 24, Appl	661	36	1.0	71	4	US-08-973-124-5	Sequence 5, Appl
C 589	37	1.0	13999	4	US-08-232-246A-24	Sequence 24, Appl	662	36	1.0	71	4	US-08-973-124-5	Sequence 5, Appl
C 590	37	1.0	14753	4	US-09-821-736-3	Sequence 3, Appl	663	36	1.0	71	5	PCT-US96-08014-5	Sequence 5, Appl
C 591	37	1.0	19806	4	US-09-740-028A-3	Sequence 3, Appl	664	36	1.0	71	5	PCT-US96-08014-5	Sequence 5, Appl
C 592	37	1.0	28001	4	US-09-819-993-3	Sequence 3, Appl	665	36	1.0	72	2	US-07-829-461A-6	Sequence 6, Appl
C 593	37	1.0	36651	4	US-09-738-894A-3	Sequence 3, Appl	666	36	1.0	72	4	US-09-197-649-5	Sequence 5, Appl
C 594	37	1.0	84495	4	US-09-797-906-3	Sequence 3, Appl	667	36	1.0	74	4	US-09-193-068-15	Sequence 15, Appl
C 595	37	1.0	84495	4	US-09-797-906-3	Sequence 3, Appl	668	36	1.0	75	1	US-08-437-815-10	Sequence 10, Appl
C 596	37	1.0	111282	4	US-09-754-250-3	Sequence 3, Appl	669	36	1.0	75	1	US-08-897-040-10	Sequence 10, Appl
C 597	37	1.0	112132	4	US-09-741-150-3	Sequence 3, Appl	670	36	1.0	76	4	US-09-287-936-1	Sequence 1, Appl
C 598	36	1.0	37	1	US-08-162-590A-5	Sequence 5, Appl	671	36	1.0	76	5	PCT-US95-05600-1	Sequence 1, Appl
C 599	36	1.0	37	1	US-08-162-590A-5	Sequence 5, Appl	672	36	1.0	78	4	US-09-193-068-17	Sequence 17, Appl
C 600	36	1.0	37	1	US-08-162-590A-6	Sequence 6, Appl	673	36	1.0	80	1	US-08-471-985A-112	Sequence 112, App
C 601	36	1.0	37	1	US-08-162-590A-6	Sequence 6, Appl	674	36	1.0	80	1	US-08-471-985A-112	Sequence 112, App
C 602	36	1.0	37	1	US-08-162-590A-7	Sequence 7, Appl	675	36	1.0	80	1	US-08-472-255A-126	Sequence 126, App
C 603	36	1.0	37	1	US-08-162-590A-7	Sequence 7, Appl	676	36	1.0	80	1	US-08-472-255A-126	Sequence 126, App
C 604	36	1.0	37	1	US-08-162-590A-8	Sequence 8, Appl	677	36	1.0	80	1	US-08-479-724A-126	Sequence 126, App
C 605	36	1.0	37	1	US-08-162-590A-8	Sequence 8, Appl	678	36	1.0	80	1	US-08-479-724A-126	Sequence 126, App
C 606	36	1.0	39	2	US-08-659-453B-2	Sequence 2, Appl	679	36	1.0	80	1	US-08-472-194A-4	Sequence 4, Appl
C 607	36	1.0	39	3	US-09-089-853A-2	Sequence 2, Appl	680	36	1.0	80	1	US-08-418-859-47	Sequence 47, Appl
C 608	36	1.0	39	4	US-09-131-009A-2	Sequence 2, Appl	681	36	1.0	80	1	US-08-418-859-47	Sequence 47, Appl
C 609	36	1.0	39	4	US-09-092-226A-2	Sequence 2, Appl	682	36	1.0	80	2	US-08-643-181-47	Sequence 47, Appl
C 610	36	1.0	39	4	US-09-130-862A-2	Sequence 2, Appl	683	36	1.0	80	2	US-08-643-181-47	Sequence 47, Appl
C 611	36	1.0	39	4	US-09-275-850-340	Sequence 340, App	684	36	1.0	80	3	US-08-472-256B-126	Sequence 126, App

c 685	36	1.0	80	3	US-08-472-256B-126	Sequence 126, App	c 758	36	1.0	98	1	US-08-447-172A-28	Sequence 28, Appl
c 686	36	1.0	80	4	US-09-193-068-23	Sequence 23, Appl	c 759	36	1.0	98	1	US-08-447-172A-31	Sequence 31, Appl
c 687	36	1.0	80	4	US-08-952-793-126	Sequence 126, App	c 760	36	1.0	98	1	US-08-472-255A-1	Sequence 1, Appl
c 688	36	1.0	80	4	US-08-952-793-126	Sequence 126, App	c 761	36	1.0	98	1	US-08-472-255A-1	Sequence 1, Appl
c 689	36	1.0	80	4	US-08-849-567A-4	Sequence 4, Appl	c 762	36	1.0	98	2	US-08-237-973-4	Sequence 4, Appl
c 690	36	1.0	80	5	PCT-US95-12401A-112	Sequence 112, App	c 763	36	1.0	98	3	US-08-472-256B-1	Sequence 1, Appl
c 691	36	1.0	80	5	PCT-US95-12401A-112	Sequence 112, App	c 764	36	1.0	98	4	US-08-952-793-1	Sequence 1, Appl
c 692	36	1.0	80	5	PCT-US95-09455A-126	Sequence 126, App	c 765	36	1.0	98	4	US-08-849-567A-50	Sequence 50, Appl
c 693	36	1.0	80	5	PCT-US96-09455A-126	Sequence 126, App	c 766	36	1.0	98	5	PCT-US96-09455A-1	Sequence 1, Appl
c 694	36	1.0	81	1	US-08-447-169A-240	Sequence 240, App	c 767	36	1.0	99	4	US-08-849-567A-51	Sequence 51, Appl
c 695	36	1.0	81	1	US-08-447-169A-240	Sequence 240, App	c 768	36	1.0	101	1	US-07-843-125-6	Sequence 6, Appl
c 696	36	1.0	81	4	US-09-193-068-19	Sequence 19, Appl	c 769	36	1.0	104	2	US-08-139-176D-2	Sequence 2, Appl
c 697	36	1.0	82	4	US-08-679-493A-14	Sequence 14, Appl	c 770	36	1.0	104	2	US-08-139-176D-3	Sequence 3, Appl
c 698	36	1.0	83	4	US-08-687-421-325	Sequence 325, App	c 771	36	1.0	104	3	US-09-041-841-2	Sequence 2, Appl
c 699	36	1.0	85	4	US-09-275-850-338	Sequence 338, App	c 772	36	1.0	104	3	US-09-041-841-3	Sequence 3, Appl
c 700	36	1.0	85	4	US-09-275-850-339	Sequence 339, App	c 773	36	1.0	105	1	US-08-213-012-52	Sequence 52, Appl
c 701	36	1.0	86	1	US-07-964-624D-43	Sequence 43, Appl	c 774	36	1.0	105	1	US-08-213-012-52	Sequence 52, Appl
c 702	36	1.0	86	1	US-08-442-062-43	Sequence 43, Appl	c 775	36	1.0	105	4	US-08-687-421-240	Sequence 240, App
c 703	36	1.0	86	1	US-08-479-783A-1	Sequence 1, Appl	c 776	36	1.0	105	4	US-08-687-421-240	Sequence 240, App
c 704	36	1.0	86	1	US-08-479-783A-1	Sequence 1, Appl	c 777	36	1.0	107	1	US-08-472-194A-23	Sequence 23, Appl
c 705	36	1.0	86	1	US-08-479-725-1	Sequence 1, Appl	c 778	36	1.0	107	1	US-08-472-194A-23	Sequence 23, Appl
c 706	36	1.0	86	1	US-08-479-725-1	Sequence 1, Appl	c 779	36	1.0	107	4	US-08-849-567A-23	Sequence 23, Appl
c 707	36	1.0	86	1	US-08-618-693-1	Sequence 1, Appl	c 780	36	1.0	107	4	US-08-849-567A-23	Sequence 23, Appl
c 708	36	1.0	86	1	US-08-618-693-1	Sequence 1, Appl	c 781	36	1.0	108	4	US-09-296-328A-15	Sequence 15, Appl
c 709	36	1.0	86	1	US-08-447-169A-237	Sequence 237, App	c 782	36	1.0	108	4	US-09-296-328A-15	Sequence 15, Appl
c 710	36	1.0	86	1	US-08-447-169A-237	Sequence 237, App	c 783	36	1.0	110	1	US-08-299-498A-3	Sequence 3, Appl
c 711	36	1.0	86	4	US-08-748-697A-43	Sequence 43, Appl	c 784	36	1.0	110	5	PCT-US95-10813-3	Sequence 3, Appl
c 712	36	1.0	86	4	US-08-687-421-322	Sequence 322, App	c 785	36	1.0	112	1	US-08-299-498A-32	Sequence 32, Appl
c 713	36	1.0	86	4	US-08-687-421-322	Sequence 322, App	c 786	36	1.0	112	5	PCT-US95-10813-32	Sequence 32, Appl
c 714	36	1.0	86	4	US-08-973-124-90	Sequence 90, App	c 787	36	1.0	117	1	US-08-458-423A-1	Sequence 1, Appl
c 715	36	1.0	86	4	US-08-973-124-90	Sequence 90, App	c 788	36	1.0	117	1	US-08-458-423A-1	Sequence 1, Appl
c 716	36	1.0	86	4	US-08-991-743C-1	Sequence 1, Appl	c 789	36	1.0	117	1	US-08-458-424B-1	Sequence 1, Appl
c 717	36	1.0	86	4	US-08-991-743C-1	Sequence 1, Appl	c 790	36	1.0	117	1	US-08-458-424B-1	Sequence 1, Appl
c 718	36	1.0	86	4	US-09-165-616-43	Sequence 43, Appl	c 791	36	1.0	117	4	US-08-973-124-1	Sequence 1, Appl
c 719	36	1.0	86	5	PCT-US96-08014-90	Sequence 90, Appl	c 792	36	1.0	117	4	US-08-973-124-1	Sequence 1, Appl
c 720	36	1.0	86	5	PCT-US96-08014-90	Sequence 90, Appl	c 793	36	1.0	117	5	PCT-US96-08014-1	Sequence 1, Appl
c 721	36	1.0	87	1	US-08-199-507B-57	Sequence 57, App	c 794	36	1.0	117	5	PCT-US96-08014-1	Sequence 1, Appl
c 722	36	1.0	87	1	US-08-199-507B-57	Sequence 57, App	c 795	36	1.0	119	4	US-08-679-493A-15	Sequence 15, Appl
c 723	36	1.0	87	1	US-08-441-828-57	Sequence 57, App	c 796	36	1.0	119	4	US-08-679-493A-15	Sequence 15, Appl
c 724	36	1.0	87	1	US-08-441-828-57	Sequence 57, App	c 797	36	1.0	120	1	US-07-843-125-4	Sequence 4, Appl
c 725	36	1.0	87	3	US-08-973-965-13	Sequence 13, Appl	c 798	36	1.0	121	4	US-09-535-754-10	Sequence 10, Appl
c 726	36	1.0	88	4	US-09-363-939A-5	Sequence 5, Appl	c 799	36	1.0	122	4	US-09-193-068-16	Sequence 16, Appl
c 727	36	1.0	88	4	US-09-363-939A-5	Sequence 5, Appl	c 800	36	1.0	122	4	US-09-193-068-16	Sequence 16, Appl
c 728	36	1.0	90	1	US-08-358-995-28	Sequence 28, App	c 801	36	1.0	123	4	US-09-535-754-9	Sequence 9, Appl
c 729	36	1.0	90	4	US-08-679-493A-17	Sequence 17, App	c 802	36	1.0	132	2	US-08-771-201-7	Sequence 7, Appl
c 730	36	1.0	93	1	US-08-370-567-27	Sequence 27, App	c 803	36	1.0	132	2	US-08-771-201-7	Sequence 7, Appl
c 731	36	1.0	93	1	US-08-438-759-27	Sequence 27, App	c 804	36	1.0	134	1	US-08-299-498A-5	Sequence 5, Appl
c 732	36	1.0	93	1	US-08-458-423A-2	Sequence 2, App	c 805	36	1.0	134	5	PCT-US95-10813-5	Sequence 5, Appl
c 733	36	1.0	93	1	US-08-458-423A-2	Sequence 2, App	c 806	36	1.0	139	4	US-08-679-493A-60	Sequence 60, Appl
c 734	36	1.0	93	1	US-08-458-424B-2	Sequence 2, App	c 807	36	1.0	141	1	US-08-375-116A-131	Sequence 131, App
c 735	36	1.0	93	1	US-08-458-424B-2	Sequence 2, App	c 808	36	1.0	141	1	US-08-375-116A-131	Sequence 131, App
c 736	36	1.0	93	1	US-08-538-911-2	Sequence 2, App	c 809	36	1.0	142	1	US-08-375-116A-130	Sequence 130, App
c 737	36	1.0	93	4	US-08-117-361C-15	Sequence 15, App	c 810	36	1.0	142	1	US-08-375-116A-130	Sequence 130, App
c 738	36	1.0	93	4	US-08-973-124-2	Sequence 2, App	c 811	36	1.0	149	3	US-08-903-139B-31	Sequence 31, App
c 739	36	1.0	93	4	US-08-973-124-2	Sequence 2, App	c 812	36	1.0	149	3	US-08-903-139B-31	Sequence 31, App
c 740	36	1.0	93	5	PCT-US94-05591-2	Sequence 2, App	c 813	36	1.0	152	2	US-08-771-201-8	Sequence 8, Appl
c 741	36	1.0	93	5	PCT-US94-05591-2	Sequence 2, App	c 814	36	1.0	152	2	US-08-771-201-8	Sequence 8, Appl
c 742	36	1.0	93	5	PCT-US94-05684-27	Sequence 27, App	c 815	36	1.0	154	2	US-08-721-684C-7	Sequence 7, Appl
c 743	36	1.0	93	5	PCT-US96-08014-2	Sequence 2, App	c 816	36	1.0	154	2	US-09-005-970-7	Sequence 7, Appl
c 744	36	1.0	94	2	US-08-771-201-6	Sequence 6, App	c 817	36	1.0	154	4	US-09-407-715-7	Sequence 7, Appl
c 745	36	1.0	95	1	US-08-458-423A-4	Sequence 4, App	c 818	36	1.0	155	3	US-08-903-139B-15	Sequence 15, Appl
c 746	36	1.0	95	1	US-08-458-423A-4	Sequence 4, App	c 819	36	1.0	155	3	US-08-903-139B-15	Sequence 15, Appl
c 747	36	1.0	95	1	US-08-458-424B-4	Sequence 4, App	c 820	36	1.0	195	4	US-09-186-276B-64	Sequence 64, Appl
c 748	36	1.0	95	1	US-08-458-424B-4	Sequence 4, App	c 821	36	1.0	195	4	US-08-842-445-64	Sequence 64, Appl
c 749	36	1.0	95	4	US-08-973-124-4	Sequence 4, App	c 822	36	1.0	195	4	US-09-186-276B-64	Sequence 64, Appl
c 750	36	1.0	95	4	US-08-973-124-4	Sequence 4, App	c 823	36	1.0	207	2	US-08-039-198B-6	Sequence 6, Appl
c 751	36	1.0	95	5	PCT-US96-08014-4	Sequence 4, App	c 824	36	1.0	208	1	US-08-375-116A-132	Sequence 132, App
c 752	36	1.0	95	5	PCT-US96-08014-4	Sequence 4, App	c 825	36	1.0	208	1	US-08-375-116A-132	Sequence 132, App
c 753	36	1.0	96	1	US-08-234-613-1	Sequence 1, App	c 826	36	1.0	212	4	US-09-574-141A-86	Sequence 86, Appl
c 754	36	1.0	96	1	US-08-753-054-19	Sequence 19, App	c 827	36	1.0	215	4	US-09-535-754-8	Sequence 8, Appl
c 755	36	1.0	96	2	US-08-237-973-1	Sequence 1, App	c 828	36	1.0	223	4	US-09-535-754-8	Sequence 8, Appl
c 756	36	1.0	98	1	US-08-234-613-4	Sequence 4, App	c 829	36	1.0	315	1	US-07-903-466-41	Sequence 41, Appl
c 757	36	1.0	98	1	US-08-399-412A-7	Sequence 7, App	c 830	36	1.0	315	1	US-07-903-466-41	Sequence 41, Appl

831	36	1.0	315	5	PCT-US93-05794-41	Sequence 41, Appl	904	1.0	1474	4	US-09-508-542-17	Sequence 17, Appl
832	36	1.0	315	5	PCT-US93-05794-41	Sequence 41, Appl	905	1.0	1495	4	US-09-364-230-11	Sequence 11, Appl
833	36	1.0	324	2	US-08-378-939-21	Sequence 21, Appl	c 906	1.0	1495	4	US-09-364-230-11	Sequence 11, Appl
834	36	1.0	324	2	US-08-378-939-21	Sequence 21, Appl	c 907	1.0	1576	5	PCT-US95-11405-34	Sequence 34, Appl
835	36	1.0	345	4	US-09-025-203-16	Sequence 17, Appl	c 908	1.0	1608	1	US-07-621-670-2	Sequence 2, Appl
836	36	1.0	348	4	US-09-672-609-18	Sequence 18, Appl	c 909	1.0	1608	1	US-07-621-670-2	Sequence 2, Appl
837	36	1.0	348	4	US-09-672-609-18	Sequence 18, Appl	c 910	1.0	1610	4	US-09-276-531-56	Sequence 56, Appl
838	36	1.0	348	4	US-09-672-609-18	Sequence 18, Appl	c 911	1.0	1610	4	US-09-276-531-56	Sequence 56, Appl
839	36	1.0	348	4	US-09-025-403A-18	Sequence 18, Appl	c 912	1.0	1651	4	US-09-484-970B-17	Sequence 17, Appl
840	36	1.0	398	4	US-09-574-141A-89	Sequence 89, Appl	c 913	1.0	1689	4	US-09-718-841-1	Sequence 1, Appl
841	36	1.0	398	4	US-09-574-141A-89	Sequence 89, Appl	c 914	1.0	1689	4	US-09-718-841-1	Sequence 1, Appl
842	36	1.0	423	2	US-08-822-028-62	Sequence 62, Appl	c 915	1.0	1713	4	US-08-753-436-1	Sequence 1, Appl
843	36	1.0	423	2	US-08-822-028-62	Sequence 62, Appl	c 916	1.0	1713	4	US-08-753-436-1	Sequence 1, Appl
844	36	1.0	423	4	US-08-479-285-62	Sequence 62, Appl	c 917	1.0	1738	3	US-09-120-365-89	Sequence 89, Appl
845	36	1.0	423	4	US-08-479-285-62	Sequence 62, Appl	c 918	1.0	1738	3	US-09-120-365-89	Sequence 89, Appl
846	36	1.0	426	2	US-08-822-028-65	Sequence 65, Appl	c 919	1.0	1750	3	US-09-120-365-90	Sequence 90, Appl
847	36	1.0	426	2	US-08-479-285-65	Sequence 65, Appl	c 920	1.0	1750	3	US-09-120-365-90	Sequence 90, Appl
848	36	1.0	479	4	US-09-254-352B-39	Sequence 39, Appl	c 921	1.0	1775	2	US-07-862-588B-5	Sequence 5, Appl
849	36	1.0	479	4	US-09-254-352B-39	Sequence 39, Appl	c 922	1.0	1775	2	US-07-862-588B-5	Sequence 5, Appl
850	36	1.0	495	2	US-08-465-380-31	Sequence 31, Appl	c 923	1.0	1782	1	US-08-374-155A-13	Sequence 13, Appl
851	36	1.0	495	2	US-08-465-380-31	Sequence 31, Appl	c 924	1.0	1782	1	US-08-374-155A-13	Sequence 13, Appl
852	36	1.0	495	2	US-08-486-397-31	Sequence 31, Appl	c 925	1.0	2030	4	US-09-484-970B-152	Sequence 152, Appl
853	36	1.0	495	2	US-08-486-397-31	Sequence 31, Appl	c 926	1.0	2030	4	US-09-484-970B-152	Sequence 152, Appl
854	36	1.0	551	2	US-08-461-965-31	Sequence 31, Appl	c 927	1.0	2087	4	US-09-484-970B-153	Sequence 153, Appl
855	36	1.0	595	4	US-08-647-368A-4	Sequence 4, Appl	c 928	1.0	2116	2	US-08-663-566A-18	Sequence 18, Appl
856	36	1.0	595	4	US-09-276-531-63	Sequence 63, Appl	c 929	1.0	2116	2	US-08-023-610-18	Sequence 18, Appl
857	36	1.0	595	4	US-09-276-531-63	Sequence 63, Appl	c 930	1.0	2116	2	US-08-288-065A-18	Sequence 18, Appl
858	36	1.0	608	1	US-08-386-495-11	Sequence 11, Appl	c 931	1.0	2116	5	PCT-US95-10245-18	Sequence 18, Appl
859	36	1.0	616	4	PCT-US96-02331-11	Sequence 11, Appl	c 932	1.0	2157	4	US-08-837-199A-15	Sequence 15, Appl
860	36	1.0	616	4	US-09-276-531-39	Sequence 39, Appl	c 933	1.0	2157	4	US-08-837-199A-15	Sequence 15, Appl
861	36	1.0	633	4	US-09-276-531-39	Sequence 39, Appl	c 934	1.0	2158	4	US-08-837-199A-43	Sequence 43, Appl
862	36	1.0	670	2	US-08-812-484-25	Sequence 25, Appl	c 935	1.0	2158	4	US-08-837-199A-43	Sequence 43, Appl
863	36	1.0	670	2	US-08-784-208-2	Sequence 2, Appl	c 936	1.0	2300	1	US-08-103-998-3	Sequence 3, Appl
864	36	1.0	699	4	US-09-276-531-91	Sequence 91, Appl	c 937	1.0	2300	1	US-08-103-998-3	Sequence 3, Appl
865	36	1.0	699	4	US-09-276-531-91	Sequence 91, Appl	c 938	1.0	2379	4	US-09-484-970B-139	Sequence 139, Appl
866	36	1.0	759	3	US-09-109-205-11	Sequence 11, Appl	c 939	1.0	2379	4	US-09-484-970B-139	Sequence 139, Appl
867	36	1.0	759	4	US-09-276-531-71	Sequence 71, Appl	c 940	1.0	2409	4	US-09-293-322C-8	Sequence 8, Appl
868	36	1.0	804	4	US-09-276-531-54	Sequence 54, Appl	c 941	1.0	2428	2	US-08-849-536A-3	Sequence 3, Appl
869	36	1.0	808	4	US-08-791-115B-12	Sequence 12, Appl	c 942	1.0	2475	4	US-09-624-593A-20	Sequence 20, Appl
870	36	1.0	830	4	US-08-387-707-13	Sequence 13, Appl	c 943	1.0	2568	4	US-08-837-199A-1	Sequence 1, Appl
871	36	1.0	830	4	US-08-387-707-13	Sequence 13, Appl	c 944	1.0	2568	4	US-08-837-199A-1	Sequence 1, Appl
872	36	1.0	830	4	US-08-405-271A-13	Sequence 13, Appl	c 945	1.0	2635	4	US-08-186-276B-57	Sequence 57, Appl
873	36	1.0	830	4	US-08-405-271A-13	Sequence 13, Appl	c 946	1.0	2635	4	US-08-186-276B-57	Sequence 57, Appl
874	36	1.0	887	4	US-09-276-531-4	Sequence 4, Appl	c 947	1.0	2635	4	US-08-842-445-57	Sequence 57, Appl
875	36	1.0	887	4	US-09-276-531-4	Sequence 4, Appl	c 948	1.0	2635	4	US-08-842-445-57	Sequence 57, Appl
876	36	1.0	959	4	US-09-724-510-1	Sequence 1, Appl	c 949	1.0	2635	4	US-09-186-188B-57	Sequence 57, Appl
877	36	1.0	959	4	US-09-723-216-1	Sequence 1, Appl	c 950	1.0	2635	4	US-09-186-188B-57	Sequence 57, Appl
878	36	1.0	959	4	US-09-675-227-1	Sequence 1, Appl	c 951	1.0	2793	1	US-08-209-747-1	Sequence 1, Appl
879	36	1.0	1070	4	US-09-718-841-3	Sequence 3, Appl	c 952	1.0	2793	1	US-08-458-288-1	Sequence 1, Appl
880	36	1.0	1070	4	US-09-718-841-3	Sequence 3, Appl	c 953	1.0	2847	4	US-09-484-970B-22	Sequence 22, Appl
881	36	1.0	1075	4	US-08-837-199A-21	Sequence 21, Appl	c 954	1.0	3083	4	US-08-956-657-1	Sequence 1, Appl
882	36	1.0	1075	4	US-08-837-199A-21	Sequence 21, Appl	c 955	1.0	3209	4	US-08-956-657-1	Sequence 1, Appl
883	36	1.0	1076	4	US-08-837-199A-46	Sequence 46, Appl	c 956	1.0	3209	4	US-08-837-199A-5	Sequence 5, Appl
884	36	1.0	1076	4	US-08-837-199A-46	Sequence 46, Appl	c 957	1.0	3209	4	US-08-837-199A-57	Sequence 57, Appl
885	36	1.0	1083	4	US-09-276-531-30	Sequence 30, Appl	c 958	1.0	3209	4	US-08-837-199A-37	Sequence 37, Appl
886	36	1.0	1083	4	US-09-276-531-30	Sequence 30, Appl	c 959	1.0	3450	4	US-08-462-561B-10	Sequence 10, Appl
887	36	1.0	1094	4	US-09-280-116-243	Sequence 243, Appl	c 960	1.0	3450	4	US-09-462-561B-10	Sequence 10, Appl
888	36	1.0	1143	4	US-09-276-531-103	Sequence 103, Appl	c 961	1.0	3720	1	US-08-074-967-1	Sequence 1, Appl
889	36	1.0	1183	2	US-08-731-723-8	Sequence 8, Appl	c 962	1.0	3720	2	US-08-553-541B-1	Sequence 1, Appl
890	36	1.0	1233	4	US-09-276-531-7	Sequence 7, Appl	c 963	1.0	3720	4	US-09-268-202-1	Sequence 1, Appl
891	36	1.0	1252	4	US-09-276-531-92	Sequence 92, Appl	c 964	1.0	3720	5	PCT-US94-06669-1	Sequence 1, Appl
892	36	1.0	1285	4	US-09-276-531-52	Sequence 52, Appl	c 965	1.0	3837	4	US-09-724-517-1	Sequence 1, Appl
893	36	1.0	1285	2	US-08-039-198B-7	Sequence 7, Appl	c 966	1.0	3837	4	US-09-724-517-1	Sequence 1, Appl
894	36	1.0	1361	4	US-09-280-116-197	Sequence 197, Appl	c 967	1.0	3837	4	US-09-641-807A-1	Sequence 1, Appl
895	36	1.0	1361	4	US-09-280-116-197	Sequence 197, Appl	c 968	1.0	3837	4	US-09-641-807A-1	Sequence 1, Appl
896	36	1.0	1461	3	US-08-445-463B-5	Sequence 5, Appl	c 969	1.0	3837	4	US-09-723-096-1	Sequence 1, Appl
897	36	1.0	1461	3	US-08-445-463B-5	Sequence 5, Appl	c 970	1.0	3837	4	US-09-723-096-1	Sequence 1, Appl
898	36	1.0	1461	3	US-08-445-464C-5	Sequence 5, Appl	c 971	1.0	3915	2	US-08-485-139-6	Sequence 6, Appl
899	36	1.0	1461	3	US-08-445-464C-5	Sequence 5, Appl	c 972	1.0	3915	2	US-08-485-139-6	Sequence 6, Appl
900	36	1.0	1461	4	US-08-044-857D-5	Sequence 5, Appl	c 973	1.0	3915	3	US-08-750-357-6	Sequence 6, Appl
901	36	1.0	1461	4	US-08-044-857D-5	Sequence 5, Appl	c 974	1.0	3915	3	US-08-750-357-6	Sequence 6, Appl
902	36	1.0	1461	5	PCT-US94-03437-5	Sequence 5, Appl	c 975	1.0	3952	2	US-08-381-691-16	Sequence 16, Appl
903	36	1.0	1461	5	PCT-US94-03437-5	Sequence 5, Appl	c 976	1.0	4201	6	5254799-3	Patent No. 5254799

C 977 36 1.0 4201 6 5254799-3
C 978 36 1.0 4339 4 US-09-484-970B-164
C 979 36 1.0 4533 3 US-08-863-790-27
C 980 36 1.0 4533 3 US-08-863-790-27
C 981 36 1.0 4533 3 US-08-296-749-27
C 982 36 1.0 4533 3 US-08-296-749-27
C 983 36 1.0 4701 3 US-08-651-472-64
C 984 36 1.0 4701 3 US-08-358-928-64
C 985 36 1.0 4772 4 US-09-484-970B-133
C 986 36 1.0 4858 4 US-09-392-184-1
C 987 36 1.0 4874 4 US-09-484-970B-36
C 988 36 1.0 4997 1 US-08-232-463-1
C 989 36 1.0 6775 4 US-09-402-929-4
C 990 36 1.0 8299 1 US-08-462-014-2
C 991 36 1.0 8299 3 US-08-923-137-3
C 992 36 1.0 8299 4 US-08-973-334-5
C 993 36 1.0 8299 4 US-09-563-869A-5
C 994 36 1.0 8313 1 US-08-232-463-2
C 995 36 1.0 8575 5 PCT-US92-08258-6
C 996 36 1.0 8575 5 PCT-US92-08258-6
C 997 36 1.0 8775 1 US-08-232-463-5
C 998 36 1.0 9454 1 US-08-232-463-3
C 999 36 1.0 9454 1 US-08-232-463-4
C1000 36 1.0 11528 3 US-08-444-644-18

ALIGNMENTS

RESULT 1
US-08-208-005C-1
; Sequence 1, Application US/08208005C
; Patent No. 5837498
; GENERAL INFORMATION:
; APPLICANT: OLSEN, ET AL.
; TITLE OF INVENTION: Corpuscles of Stannius Protein, Stanniocalcin
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/208, 005C
; FILING DATE: 8 MARCH 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: FERRARO, GREGORY D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325900-78
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 771 BASE PAIRS
; TYPE: NUCLEIC ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; MOLECULE TYPE: cDNA
US-08-208-005C-1

Query Match 19.1%; Score 720; DB 2; Length 771;
Best Local Similarity 99.9%; Pred. No. 2.4e-313;
Matches 770; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 159 GAACTTCTCAGAGAAATGCTCCAAAACCTCAGCAGTGTCTTGGTGTCTGATCAGTGTCT 218
Db 1 GAACTTCTCAGAGAAATGCTCCAAAACCTCAGCAGTGTCTTGGTGTCTGATCAGTGTCT 60
QY 219 TCTGCAACCCATGAGCGGAGAGAAATGCTGTGAGCCCGAGGAAATCCCGAGTGGCG 278
Db 61 TCTGCAACCCATGAGCGGAGAGAAATGCTGTGAGCCCGAGGAAATCCCGAGTGGCG 120
QY 279 GCTCAAAAACCTCAGCTGAAATGCTTCTTCCCTCAACAGTGTCTTACAGTGTCTGCGG 338
Db 121 GCCCAAAACCTCAGCTGAAATGCTTCTTCCCTCAACAGTGTCTTACAGTGTCTGCGG 180
QY 339 GCTTTTGTGATGCTTGGAAAACTTCCACTGTGACAGATGGGATGTATGACATCTGTAAA 398
Db 181 GCTTTTGTGATGCTTGGAAAACTTCCACTGTGACAGATGGGATGTATGACATCTGTAAA 240
QY 399 TCCTTTTGTGATGCTTGGAAAACTTCCACTGTGACAGATGGGATGTATGACATCTGTAAA 458
Db 241 TCCTTTTGTGATGCTTGGAAAACTTCCACTGTGACAGATGGGATGTATGACATCTGTAAA 300
QY 459 TTAATAATGCATCGCCCAACGGGGTCACTTCCCAAGGTCTTCTCGCCATTCGGAGGTGCTCC 518
Db 301 TTAATAATGCATCGCCCAACGGGGTCACTTCCCAAGGTCTTCTCGCCATTCGGAGGTGCTCC 360
QY 519 ACTTTTCAAAGGATGATTTGCTGAGGTGAGGAAGAGTGTCTACAGCAAGTGAATGTGTGC 578
Db 361 ACTTTTCAAAGGATGATTTGCTGAGGTGAGGAAGAGTGTCTACAGCAAGTGAATGTGTGC 420
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QY 639 TCCACAGATATAACAGACTTTGTCCGAAGCCCTGCTGGAATGTGATGAAGACACAGTC 698
Db 481 TCCACAGATATAACAGACTTTGTCCGAAGCCCTGCTGGAATGTGATGAAGACACAGTC 540
QY 699 AGCAATCAGAGACAGCTGATGGAGAAATTTGGGCTTAACATGGCCAGCTCTTCCAC 758
Db 541 AGCAATCAGAGACAGCTGATGGAGAAATTTGGGCTTAACATGGCCAGCTCTTCCAC 600
QY 759 ATCTTGACAGACAGCTGCTGCCCCAACACACACAGCTGACTTCAACAGGAGAGCG 818
Db 601 ATCTTGACAGACAGCTGCTGCCCCAACACACACAGCTGACTTCAACAGGAGAGCG 660
QY 819 ACCAATGAGCGGAGAGCTGAAAGTCTCTCTCAGGAACCTCCGAGGTGAGGAGACTCT 878
Db 661 ACCAATGAGCGGAGAGCTGAAAGTCTCTCTCAGGAACCTCCGAGGTGAGGAGACTCT 720
QY 879 CCCTCCACATCAAAACGACATCCCATGAGAGTGTATTAACCGGAGAGGT 929
Db 721 CCCTCCACATCAAAACGACATCCCATGAGAGTGTATTAACCGGAGAGGT 771

RESULT 2

US-09-038-597A-1
; Sequence 1, Application US/09038597A
; Patent No. 5877290
; GENERAL INFORMATION:
; APPLICANT: OLSEN, ET AL.
; TITLE OF INVENTION: Corpuscles of Stannius Protein,
; TITLE OF INVENTION: Stanniocalcin
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA

ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/038,597A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/208,005
FILING DATE: 8-MARCH-1994
ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-78
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 771 BASE PAIRS
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
MOLECULE TYPE: cdna
US-09-038-597A-1

Query Match
Best Local Similarity 19.1%; Score 720; DB 2; Length 771;
Matches 770; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 159 GAACTTCTCAGAGATGCTCCAAACTCAGCAGTCTTCTGCTGCTGATCAGTCT 218
DB 1 GAACTTCTCAGAGATGCTCCAAACTCAGCAGTCTTCTGCTGCTGATCAGTCT 60

QY 219 TCTGCAACCCATGAGCGGAGCAGAAATGACTCTGTGACCCAGGAAATCCGAGTGGC 278
DB 61 TCTGCAACCCATGAGCGGAGCAGAAATGACTCTGTGACCCAGGAAATCCGAGTGGC 120

QY 279 GCTCAAACTCAGCTGAGTGGTTCGTTGCTCAACAGTCTCTACAGTGGCTTCCAC 758
DB 121 GCCCAAACTCAGCTGAGTGGTTCGTTGCTCAACAGTCTCTACAGTGGCTTCCAC 180

QY 339 GCTTTTGCATGCTGGAATACTCCACTGTGACAGATGGGATGATGACATCTGTAA 398
DB 181 GCTTTTGCATGCTGGAATACTCCACTGTGACAGATGGGATGATGACATCTGTAA 240

QY 399 TCTTCTTGTACAGCGCTCTAAATTGACACTCAGGGAAGAGCATTCTCAAGAGAGC 458
DB 241 TCTTCTTGTACAGCGCTCTAAATTGACACTCAGGGAAGAGCATTCTCAAGAGAGC 300

QY 459 TTAATATGATCGCCACCGGCTCACTTCAAGTCTTCTGCTGCTGAGTGGTCTCC 518
DB 301 TTAATATGATCGCCACCGGCTCACTTCAAGTCTTCTGCTGCTGAGTGGTCTCC 360

QY 519 ACTTTTCAAGATGATCTGAGGTGAGGAGAGTGTACAGCAAGCTGAATGTGTC 578
DB 361 ACTTTTCAAGATGATCTGAGGTGAGGAGAGTGTACAGCAAGCTGAATGTGTC 420

QY 579 AGCATCGCAAGCGGAACCTTGAAGCCTCACTGAGGTGCTGAGTGGTCCCAATCATT 638
DB 421 AGCATCGCAAGCGGAACCTTGAAGCCTCACTGAGGTGCTGAGTGGTCCCAATCATT 480

QY 639 TCAACAGATATATAGAGCTTGTCCGAAGCTGCTGGAATGTGATGAAGACAGCTC 698
DB 481 TCAACAGATATATAGAGCTTGTCCGAAGCTGCTGGAATGTGATGAAGACAGCTC 540

QY 699 AGCACAATCAGAGACAGCTGTGAGGAAATTTGGCCCTTAACATGCGGAGCTCTTCCAC 758
DB 541 AGCACAATCAGAGACAGCTGTGAGGAAATTTGGCCCTTAACATGCGGAGCTCTTCCAC 600

QY 759 ATCTGCGAGACAGACCACTGTGCCCCAAACACACCCACGAGCTGACTTCAACAGGAGAGC 818
DB 601 ATCTGCGAGACAGACCACTGTGCCCCAAACACACCCACGAGCTGACTTCAACAGGAGAGC 660

QY 819 ACCAATGAGCGCAGAACTGAAAGTCTCTCAGGAACCTCCGAGGTGAGGAGACTCT 878
DB 661 ACCAATGAGCGCAGAACTGAAAGTCTCTCAGGAACCTCCGAGGTGAGGAGACTCT 720

QY 879 CCCTCCACATCAACGCGACATCCCATGAGATGAGTGCATCAACCCAGGAGAGGT 929
DB 721 CCCTCCACATCAACGCGACATCCCATGAGATGAGTGCATCAACCCAGGAGAGGT 771

RESULT 3
US-08-431-117A-1
Sequence 1, Application US/08431117A
Patent No. 5994301
GENERAL INFORMATION:
APPLICANT: OLSEN, ET AL.
TITLE OF INVENTION: Corpuscles of Stannius Protein, Stanniocalcin
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/431,117A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/208,005
FILING DATE: 8 MARCH 1994
ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-296
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 771 BASE PAIRS
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
MOLECULE TYPE: cdna
US-08-431-117A-1

Query Match
Best Local Similarity 19.1%; Score 720; DB 2; Length 771;
Matches 770; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 159 GAACTTCTCAGAGATGCTCCAAACTCAGCAGTCTTCTGCTGCTGATCAGTCT 218
DB 1 GAACTTCTCAGAGATGCTCCAAACTCAGCAGTCTTCTGCTGCTGATCAGTCT 60

QY 219 TCTGCAACCCATGAGCGGAGCAGAAATGACTCTGTGACCCAGGAAATCCGAGTGGC 278
DB 61 TCTGCAACCCATGAGCGGAGCAGAAATGACTCTGTGACCCAGGAAATCCGAGTGGC 120

QY 279 GCTCAAACTCAGCTGAGTGGTTCGTTGCTCAACAGTCTCTACAGTGGCTTCCAC 338
DB 121 GCCCAAACTCAGCTGAGTGGTTCGTTGCTCAACAGTCTCTACAGTGGCTTCCAC 180

339 GCTTTTGATCGCTGGAACCTCCACCTGTGACACAGATGGGATGATGACATCTGTAA 398
 181 GCTTTTGATCGCTGGAACCTCCACCTGTGACACAGATGGGATGATGACATCTGTAA 240
 399 TCTTTCTGTACAGCGCTGCTAAATTTGACACTCAGGGAAGCAATTCCTCAAGAGAGC 458
 241 TCTTTCTGTACAGCGCTGCTAAATTTGACACTCAGGGAAGCAATTCCTCAAGAGAGC 300
 459 TTAATATGATCGCCCAACGGGTCACTCAAGGTCTTCTGCCATTCGGAGGTGCTCC 518
 301 TTAATATGATCGCCCAACGGGTCACTCAAGGTCTTCTGCCATTCGGAGGTGCTCC 360
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 421 AGCATCGCAAGCGGAACCTGAAGCCATCACTGAGGTGCTCCAGTGCCTCCCAATCTTC 480
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 721 CCTCCACATCAACGCGACATCCCATGAGATGATGATCAACACGAGAGAGT 771

RESULT 4
 US-09-738-894A-3
 ; Sequence 3, Application US/09738894A
 ; Patent No. 6331423
 ; GENERAL INFORMATION:
 ; APPLICANT: GUEGLER, Karl et al
 ; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
 ; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
 ; TITLE OF INVENTION: THEREOF
 ; FILE REFERENCE: CL000636
 ; CURRENT APPLICATION NUMBER: US/09/738,894A
 ; CURRENT FILING DATE: 2000-12-18
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 3
 ; LENGTH: 36651
 ; TYPE: DNA
 ; ORGANISM: Human
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (1)-(36651)
 ; OTHER INFORMATION: n = A,T,C or G
 US-09-738-894A-3

Query Match 1.1%; Score 41; DB 4; Length 36651;
 Best Local Similarity 100.0%; Pred. No. 4.5e-09;
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2365 AGAAAAAANNN 2405
 Db 24831 AGAAAAAANNN 24871

RESULT 5
 US-08-679-493A-18
 ; Sequence 18, Application US/08679493A
 ; Patent No. 6303295
 ; GENERAL INFORMATION:
 ; APPLICANT: Taylor, Ethan W.
 ; TITLE OF INVENTION: SELENOPROTEINS, CODING SEQUENCES AND METHODS
 ; FILE REFERENCE: 55-95
 ; CURRENT APPLICATION NUMBER: US/08/679,493A
 ; CURRENT FILING DATE: 1996-07-12
 ; PRIOR APPLICATION NUMBER: 60/001203
 ; PRIOR FILING DATE: 1995-07-14
 ; PRIOR APPLICATION NUMBER: 60/003,112
 ; PRIOR FILING DATE: 1995-09-01
 ; NUMBER OF SEQ ID NOS: 216
 ; SOFTWARE: Patent In Ver. 2.0
 ; SEQ ID NO 18
 ; LENGTH: 99
 ; TYPE: RNA
 ; ORGANISM: Visna virus
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (1)-(99)
 ; OTHER INFORMATION: N is A, U, G or C.
 US-08-679-493A-18

Query Match 1.1%; Score 40; DB 4; Length 99;
 Best Local Similarity 100.0%; Pred. No. 1.9e-08;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2366 GAAANNN 2405
 Db 27 GAAANNN 66

RESULT 6
 US-09-800-960-3/c
 ; Sequence 3, Application US/09800960
 ; Patent No. 6387677
 ; GENERAL INFORMATION:
 ; APPLICANT: YE, Jane et al.
 ; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
 ; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
 ; TITLE OF INVENTION: THEREOF
 ; FILE REFERENCE: CL001158
 ; CURRENT APPLICATION NUMBER: US/09/800,960
 ; CURRENT FILING DATE: 2001-03-08
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 3
 ; LENGTH: 62804
 ; TYPE: DNA
 ; ORGANISM: Human
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (1)-(62804)
 ; OTHER INFORMATION: n = A,T,C or G
 US-09-800-960-3

Query Match 1.1%; Score 40; DB 4; Length 62804;
 Best Local Similarity 100.0%; Pred. No. 1.2e-08;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2370 NNNCTGG 2409
 Db 393 NNNCTGG 354

RESULT 7
 US-08-659-453B-4/c
 ; Sequence 4, Application US/08659453B
 ; Patent No. 5846719

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COMPUTER: IBM compatible  
OPERATING SYSTEM: Windows 98  
SOFTWARE: Microsoft Word2000  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/089,853A  
FILING DATE: 03-JUN-98  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/659,453  
FILING DATE: 06-JUN-96  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/358,810  
FILING DATE: 19-DEC-94  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/322,348  
FILING DATE: 13-OCT-94  
ATTORNEY/AGENT INFORMATION:  
NAME: Stephen C. Macevicz  
REGISTRATION NUMBER: 30,285  
REFERENCE/DOCKET NUMBER: 802-11  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (510) 670-9365  
TELEFAX: (510) 670-9302  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 62 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
US-09-089-853A-4
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Query Match 1.0%; Score 39; DB 3; Length 62;
Best Local Similarity 100.0%; Pred. No. 5.6e-08;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2367 AAANN 2405
DB 46 AA 8

RESULT 9

US-09-131-009A-4/c
Sequence 4, Application US/09131009A
Patent No. 6172214
Patent No. 6172214 6171856
GENERAL INFORMATION:
APPLICANT: Sydney Brenner, Glenn Albrecht, Stephen C. Macevicz
TITLE OF INVENTION: Oligonucleotide fags for Sorting and Identification
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSER: Stephen C. Macevicz, Lynx Therapeutics, Inc.
STREET: 25861 Industrial Blvd.
CITY: Hayward
STATE: California
COUNTRY: USA
ZIP: 94545
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: Windows 98
SOFTWARE: Microsoft Word2000
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/131,009A
FILING DATE: 06-AUG-98
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/659,453
FILING DATE: 06-JUN-96
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/358,810
FILING DATE: 19-DEC-94
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/322,348

NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Stephen C. Macevicz, Lynx Therapeutics, Inc.
STREET: 25861 Industrial Blvd.
CITY: Hayward
STATE: California
COUNTRY: USA
ZIP: 94545
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: Windows 98
SOFTWARE: Microsoft Word2000
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/090,809A
FILING DATE: 04-JUN-98
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/559,453
FILING DATE: 06-JUN-96
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/358,810
FILING DATE: 19-DEC-94
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/322,348
FILING DATE: 13-OCT-94
ATTORNEY/AGENT INFORMATION:
NAME: Stephen C. Macevicz
REGISTRATION NUMBER: 30,285
REFERENCE/DOCKET NUMBER: 802-08
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 670-9365
TELEFAX: (510) 670-9302
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 62 nucleotides
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-09-090-809A-4

Query Match 1.0%; Score 39; DB 4; Length 62;
Best Local Similarity 100.0%; Pred. No. 5.6e-08;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2367 AA 2405
Db 46 AA 8

RESULT 13
US-09-053-116A-4/c
Sequence 4, Application US/09053116A
Patent No. 6352828
GENERAL INFORMATION:
APPLICANT: Sydney Brenner, Glenn Albrecht, Stephen C. Macevicz
TITLE OF INVENTION: Oligonucleotide Tags for Sorting and Identification
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Stephen C. Macevicz, Spectragen, Inc.
STREET: 3832 Bay Center Place
CITY: Hayward
STATE: California
COUNTRY: USA
ZIP: 94545
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Microsoft Word 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/053,116A
FILING DATE: 01-Apr-1998

CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/659,453
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/478,238
FILING DATE: 07-JUN-95
APPLICATION NUMBER: 08/485,105
FILING DATE: 07-JUN-95
APPLICATION NUMBER: PCT/US95/12791
FILING DATE: 12-OCT-95
ATTORNEY/AGENT INFORMATION:
NAME: Stephen C. Macevicz
REGISTRATION NUMBER: 30,285
REFERENCE/DOCKET NUMBER: cbd4wo
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 670-9365
TELEFAX: (510) 670-9302
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 62 nucleotides
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-053-116A-4

Query Match 1.0%; Score 39; DB 4; Length 62;
Best Local Similarity 100.0%; Pred. No. 5.6e-08;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2367 AA 2405
Db 46 AA 8

RESULT 14
US-08-659-453B-1/c
Sequence 1, Application US/08659453B
Patent No. 5846719
GENERAL INFORMATION:
APPLICANT: Sydney Brenner, Glenn Albrecht, Stephen C. Macevicz
TITLE OF INVENTION: Oligonucleotide Tags for Sorting and Identification
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Stephen C. Macevicz, Spectragen, Inc.
STREET: 3832 Bay Center Place
CITY: Hayward
STATE: California
COUNTRY: USA
ZIP: 94545
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Microsoft Word 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/659,453B
FILING DATE: 06-JUN-96
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/12791
FILING DATE: 12-OCT-95
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/478,238
FILING DATE: 07-JUN-95
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/485,105
FILING DATE: 07-JUN-95
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/12791
FILING DATE: 12-OCT-95
ATTORNEY/AGENT INFORMATION:
NAME: Stephen C. Macevicz

REGISTRATION NUMBER: 30,285
REFERENCE/DOCKET NUMBER: cbd4wo
TELEPHONE: (510) 670-9365
TELEFAX: (510) 670-9302
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 66 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-659-453B-1

Query Match 1.0%; Score 39; DB 2; Length 66;
Best Local Similarity 100.0%; Pred. No. 5.6e-08;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2367 AA 2405
Db 50 AA 12

RESULT 15

US-09-089-853A-1/c
Sequence 1, Application US/09089853A
Patent No. 6138077

GENERAL INFORMATION:

APPLICANT: Sydney Brenner, Stephen C. Macevitz
TITLE OF INVENTION: A Method, Apparatus and Computer Program Product for Determining
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Stephen C. Macevitz, Lynx Therapeutics, Inc.
STREET: 25861 Industrial Blvd.
CITY: Hayward
STATE: California
COUNTRY: USA
ZIP: 94545

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: Windows 98
SOFTWARE: Microsoft Word2000
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/089,853A
FILING DATE: 03-JUN-98
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/659,453
FILING DATE: 06-JUN-96
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/358,810
FILING DATE: 19-DEC-94
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/322,348
FILING DATE: 13-OCT-94

ATTORNEY/AGENT INFORMATION:
NAME: Stephen C. Macevitz
REGISTRATION NUMBER: 30,285
REFERENCE/DOCKET NUMBER: 802-11
TELEPHONE: (510) 670-9365
TELEFAX: (510) 670-9302
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 66 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-09-089-853A-1

Query Match 1.0%; Score 39; DB 3; Length 66;
Best Local Similarity 100.0%; Pred. No. 5.6e-08;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2367 AA 2405
Db 50 AA 12

Search completed: June 12, 2003, 17:03:14
Job time : 211 secs

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94	39	1.0	1203	9	US-10-011-585A-42	Sequence 42, Appl	167	39	1.0	19217	10	US-09-955-866-18	Sequence 18, Appl
95	39	1.0	1222	9	US-10-011-585A-43	Sequence 43, Appl	c 168	39	1.0	19217	10	US-09-955-866-18	Sequence 18, Appl
96	39	1.0	1302	9	US-10-245-103-69	Sequence 69, Appl	c 169	39	1.0	21222	10	US-09-734-676-3	Sequence 3, Appli
97	39	1.0	1302	9	US-10-245-107-69	Sequence 69, Appl	c 170	39	1.0	23668	9	US-10-254-577-3	Sequence 3, Appli
98	39	1.0	1302	9	US-10-245-143-69	Sequence 69, Appl	c 171	39	1.0	23668	10	US-09-741-148A-3	Sequence 3, Appli
99	39	1.0	1302	9	US-10-245-147-69	Sequence 69, Appl	c 172	39	1.0	26320	9	US-10-166-221-3	Sequence 3, Appli
100	39	1.0	1302	9	US-10-245-771-69	Sequence 69, Appl	c 173	39	1.0	30676	10	US-09-927-091-8	Sequence 8, Appli
101	39	1.0	1302	9	US-10-245-851-69	Sequence 69, Appl	c 174	39	1.0	31129	9	US-10-298-192-3	Sequence 3, Appli
102	39	1.0	1302	9	US-10-237-583-69	Sequence 69, Appl	c 175	39	1.0	31766	9	US-10-288-478-5	Sequence 5, Appli
103	39	1.0	1302	9	US-10-238-183-69	Sequence 69, Appl	c 176	39	1.0	31766	10	US-09-765-344-5	Sequence 5, Appli
104	39	1.0	1302	9	US-10-238-283-69	Sequence 69, Appl	c 177	39	1.0	36159	12	US-10-135-687-3	Sequence 3, Appli
105	39	1.0	1302	9	US-10-238-370-69	Sequence 69, Appl	c 178	39	1.0	40090	10	US-09-820-004-3	Sequence 3, Appli
106	39	1.0	1302	9	US-10-245-055-69	Sequence 69, Appl	c 179	39	1.0	41104	10	US-09-816-685-3	Sequence 3, Appli
107	39	1.0	1302	9	US-10-245-147-69	Sequence 69, Appl	c 180	39	1.0	64467	9	US-10-274-409-3	Sequence 3, Appli
108	39	1.0	1302	9	US-10-245-730-69	Sequence 69, Appl	c 181	39	1.0	65464	9	US-09-859-888-3	Sequence 3, Appli
109	39	1.0	1302	9	US-10-245-739-69	Sequence 69, Appl	c 182	39	1.0	78785	9	US-09-978-167-3	Sequence 3, Appli
110	39	1.0	1302	9	US-10-246-210-69	Sequence 69, Appl	c 183	39	1.0	96649	9	US-09-956-712-10	Sequence 10, Appl
111	39	1.0	1302	9	US-10-239-196-69	Sequence 69, Appl	c 184	39	1.0	98829	9	US-10-017-724-3	Sequence 3, Appli
112	39	1.0	1302	9	US-10-243-024-69	Sequence 69, Appl	c 185	39	1.0	106323	10	US-10-300-827-3	Sequence 3, Appli
113	39	1.0	1302	9	US-10-243-409-69	Sequence 69, Appl	c 186	39	1.0	106323	10	US-09-803-661-3	Sequence 3, Appli
114	39	1.0	1302	9	US-10-245-033-69	Sequence 69, Appl	c 187	39	1.0	147309	10	US-09-742-312-3	Sequence 3, Appli
115	39	1.0	1302	9	US-10-245-621-69	Sequence 69, Appl	c 188	39	1.0	147309	10	US-09-742-312-3	Sequence 3, Appli
116	39	1.0	1302	9	US-10-245-880-69	Sequence 69, Appl	c 189	39	1.0	172637	10	US-09-835-232-6	Sequence 7, Appli
117	39	1.0	1302	9	US-10-243-095-69	Sequence 69, Appl	c 190	39	1.0	172637	10	US-09-805-458A-3	Sequence 3, Appli
118	39	1.0	1302	9	US-10-245-185-69	Sequence 69, Appl	c 191	39	1.0	180216	10	US-09-835-232-6	Sequence 6, Appli
119	39	1.0	1302	9	US-10-245-427-69	Sequence 69, Appl	c 192	39	1.0	202001	9	US-10-274-990-3	Sequence 3, Appli
120	39	1.0	1302	9	US-10-245-473-69	Sequence 69, Appl	c 193	39	1.0	202001	10	US-09-734-674-3	Sequence 3, Appli
121	39	1.0	1302	9	US-10-245-770-69	Sequence 69, Appl	c 194	39	1.0	203654	10	US-09-820-905-3	Sequence 3, Appli
122	39	1.0	1302	9	US-10-245-877-69	Sequence 69, Appl	c 195	39	1.0	254366	9	US-09-822-871-3	Sequence 3, Appli
123	39	1.0	1302	9	US-10-246-976-69	Sequence 69, Appl	c 196	39	1.0	378361	9	US-09-901-136-3	Sequence 3, Appli
124	39	1.0	1302	9	US-10-243-320-69	Sequence 69, Appl	c 197	39	1.0	397658	10	US-09-813-320-3	Sequence 3, Appli
125	39	1.0	1302	9	US-10-242-743-69	Sequence 69, Appl	c 198	39	1.0	61	9	US-09-907-111-291	Sequence 291, App
126	39	1.0	1302	9	US-10-242-845-69	Sequence 69, Appl	c 199	39	1.0	75	10	US-09-833-381-884	Sequence 884, App
127	39	1.0	1304	10	US-09-833-381-1137	Sequence 1137, Ap	c 200	38	1.0	86	10	US-09-781-902-63	Sequence 63, Appl
128	39	1.0	1647	10	US-09-833-381-862	Sequence 862, App	c 201	38	1.0	87	9	US-09-916-443A-2	Sequence 2, Appli
129	39	1.0	1814	10	US-09-955-866-17	Sequence 17, Appl	c 202	38	1.0	87	9	US-09-916-443A-2	Sequence 2, Appli
130	39	1.0	1901	9	US-10-002-344A-130	Sequence 130, App	c 203	38	1.0	87	12	US-10-096-830-44	Sequence 44, Appl
131	39	1.0	2002	10	US-09-778-844-66	Sequence 66, Appl	c 204	38	1.0	87	12	US-10-096-830-44	Sequence 44, Appl
132	39	1.0	2209	10	US-09-726-397A-2	Sequence 2, Appli	c 205	38	1.0	90	10	US-09-780-929-100	Sequence 100, App
133	39	1.0	2266	10	US-09-726-397A-3	Sequence 3, Appli	c 206	38	1.0	96	9	US-09-851-486-36	Sequence 36, Appl
134	39	1.0	2475	10	US-09-939-408A-20	Sequence 20, Appl	c 207	38	1.0	96	9	US-09-851-486-36	Sequence 36, Appl
135	39	1.0	2591	9	US-10-198-846-13636	Sequence 13636, A	c 208	38	1.0	97	9	US-10-066-960-248	Sequence 248, App
136	39	1.0	3032	10	US-09-833-381-1482	Sequence 1482, Ap	c 209	38	1.0	97	9	US-10-066-960-248	Sequence 248, App
137	39	1.0	3032	10	US-09-833-381-1483	Sequence 1483, Ap	c 210	38	1.0	97	9	US-10-066-960-248	Sequence 248, App
138	39	1.0	3075	10	US-09-833-381-1947	Sequence 1947, Ap	c 211	38	1.0	97	9	US-10-066-960-248	Sequence 248, App
139	39	1.0	3083	10	US-09-780-114-1	Sequence 1, Appli	c 212	38	1.0	97	9	US-09-849-928-248	Sequence 248, App
140	39	1.0	3110	9	US-10-198-846-9938	Sequence 9938, Ap	c 213	38	1.0	97	9	US-09-849-928-248	Sequence 248, App
141	39	1.0	3114	10	US-09-833-381-1372	Sequence 1372, Ap	c 214	38	1.0	97	9	US-09-849-928-248	Sequence 248, App
142	39	1.0	3210	9	US-09-989-920-122	Sequence 122, App	c 215	38	1.0	97	9	US-09-849-928-248	Sequence 248, App
143	39	1.0	3720	10	US-09-107-058-1	Sequence 1, Appli	c 216	38	1.0	97	10	US-09-780-929-102	Sequence 102, App
144	39	1.0	3720	10	US-09-761-117-1	Sequence 1, Appli	c 217	38	1.0	103	9	US-09-952-680A-4	Sequence 4, Appli
145	39	1.0	3811	9	US-10-198-846-12380	Sequence 12380, A	c 218	38	1.0	104	12	US-10-024-997-1	Sequence 1, Appli
146	39	1.0	3970	9	US-10-158-646-9	Sequence 9, Appli	c 219	38	1.0	104	12	US-10-024-997-1	Sequence 1, Appli
147	39	1.0	4158	10	US-09-349-015-34	Sequence 34, Appl	c 220	38	1.0	123	9	US-09-781-902-55	Sequence 55, Appl
148	39	1.0	4428	10	US-09-833-381-1364	Sequence 1364, Ap	c 221	38	1.0	128	9	US-09-952-680A-1	Sequence 1, Appli
149	39	1.0	4733	9	US-10-198-846-11332	Sequence 11332, A	c 222	38	1.0	147	9	US-09-916-443A-6	Sequence 6, Appli
150	39	1.0	5866	12	US-10-044-090-215	Sequence 215, App	c 223	38	1.0	147	9	US-09-916-443A-6	Sequence 6, Appli
151	39	1.0	6426	9	US-09-316-622-3	Sequence 3, Appli	c 224	38	1.0	147	9	US-09-916-443A-7	Sequence 7, Appli
152	39	1.0	6500	9	US-09-316-622-4	Sequence 4, Appli	c 225	38	1.0	147	9	US-09-916-443A-7	Sequence 7, Appli
153	39	1.0	6542	9	US-10-198-846-9801	Sequence 9801, Ap	c 226	38	1.0	217	9	US-10-082-830-29	Sequence 29, Appl
154	39	1.0	6652	12	US-10-044-090-762	Sequence 762, App	c 227	38	1.0	223	10	US-10-108-077-7	Sequence 7, Appli
155	39	1.0	6750	9	US-09-316-622-2	Sequence 2, Appli	c 228	38	1.0	223	10	US-09-867-262-6	Sequence 6, Appli
156	39	1.0	7074	9	US-09-316-622-1	Sequence 1, Appli	c 229	38	1.0	223	10	US-09-885-551A-7	Sequence 7, Appli
157	39	1.0	9000	9	US-09-949-427-3	Sequence 3, Appli	c 230	38	1.0	223	12	US-10-087-426-7	Sequence 7, Appli
158	39	1.0	10100	9	US-09-316-622-5	Sequence 5, Appli	c 231	38	1.0	233	10	US-09-872-153-8	Sequence 8, Appli
159	39	1.0	10166	9	US-09-316-622-8	Sequence 8, Appli	c 232	38	1.0	258	12	US-10-006-773-7	Sequence 7, Appli
160	39	1.0	10240	9	US-09-316-622-6	Sequence 6, Appli	c 233	38	1.0	275	10	US-09-294-0938-290	Sequence 290, App
161	39	1.0	10372	9	US-09-316-622-7	Sequence 7, Appli	c 234	38	1.0	281	9	US-10-011-585A-55	Sequence 55, Appl
162	39	1.0	13608	10	US-09-861-846-3	Sequence 3, Appli	c 235	38	1.0	282	9	US-10-016-634A-30	Sequence 30, Appl
163	39	1.0	13608	10	US-09-861-846-3	Sequence 3, Appli	c 236	38	1.0	284	10	US-09-294-0938-2241	Sequence 2241, Ap
164	39	1.0	15515	10	US-09-822-860-3	Sequence 3, Appli	c 237	38	1.0	290	10	US-09-294-0938-4960	Sequence 4960, Ap
165	39	1.0	17138	12	US-10-014-501-3	Sequence 3, Appli	c 238	38	1.0	303	9	US-09-989-920-110	Sequence 110, App

239	38	1.0	390	9	US-10-016-157A-131	Sequence 131, App	c 312	38	1.0	1307	10	US-09-995-494-66	Sequence 66, Appl
240	38	1.0	397	9	US-10-198-846-10914	Sequence 10914, A	313	38	1.0	1339	10	US-09-778-844-73	Sequence 73, Appl
241	38	1.0	418	10	US-09-833-381-785	Sequence 785, App	314	38	1.0	1433	9	US-10-198-846-4247	Sequence 4247, Ap
242	38	1.0	427	10	US-09-886-241-3	Sequence 3, Appl	315	38	1.0	1435	9	US-10-016-157A-87	Sequence 87, Appl
243	38	1.0	451	9	US-09-918-995-24108	Sequence 24108, A	316	38	1.0	1461	9	US-10-198-846-13947	Sequence 13947, A
244	38	1.0	480	10	US-09-771-209-35	Sequence 35, Appl	317	38	1.0	1619	9	US-10-198-846-13876	Sequence 13876, A
245	38	1.0	483	10	US-09-895-686-36	Sequence 36, Appl	318	38	1.0	1626	9	US-10-198-846-13819	Sequence 13819, A
246	38	1.0	488	9	US-09-918-995-15307	Sequence 15307, A	c 319	38	1.0	1704	9	US-10-011-445-41	Sequence 41, Appl
247	38	1.0	502	9	US-10-011-445-24	Sequence 24, Appl	320	38	1.0	1734	10	US-09-349-015-23	Sequence 23, Appl
248	38	1.0	502	9	US-09-918-995-1333	Sequence 1333, Ap	321	38	1.0	1740	10	US-09-349-015-30	Sequence 30, Appl
249	38	1.0	502	9	US-09-918-995-19713	Sequence 19713, A	322	38	1.0	1753	12	US-10-044-090-314	Sequence 314, App
250	38	1.0	509	9	US-09-918-995-23157	Sequence 23157, A	323	38	1.0	1810	10	US-09-833-381-1056	Sequence 1056, Ap
251	38	1.0	535	9	US-09-292-758-76	Sequence 76, Appl	324	38	1.0	1815	10	US-09-771-382-22	Sequence 22, Appl
252	38	1.0	557	9	US-09-918-995-23207	Sequence 23207, A	325	38	1.0	1824	9	US-10-198-846-11256	Sequence 11256, A
253	38	1.0	564	9	US-10-198-846-10780	Sequence 10780, A	326	38	1.0	1833	9	US-10-071-766-95	Sequence 95, Appl
254	38	1.0	570	9	US-10-158-646-8	Sequence 8, Appl	327	38	1.0	2002	10	US-09-778-844-66	Sequence 66, Appl
255	38	1.0	570	9	US-10-158-646-8	Sequence 8, Appl	328	38	1.0	2033	9	US-10-198-846-9925	Sequence 9925, Ap
256	38	1.0	594	10	US-09-812-102-77	Sequence 77, Appl	c 329	38	1.0	2141	9	US-09-784-554B-5	Sequence 5, Appl
257	38	1.0	598	9	US-10-198-846-8956	Sequence 8956, Ap	330	38	1.0	2146	9	US-10-071-766-83	Sequence 83, Appl
258	38	1.0	607	9	US-10-198-846-8124	Sequence 8124, Ap	331	38	1.0	2202	9	US-10-198-846-13731	Sequence 13731, A
259	38	1.0	608	9	US-10-198-846-8643	Sequence 8643, Ap	332	38	1.0	2220	9	US-10-117-846-13	Sequence 13, Appl
260	38	1.0	612	9	US-10-198-846-8479	Sequence 8479, Ap	333	38	1.0	2288	9	US-10-198-846-10854	Sequence 10854, A
261	38	1.0	617	9	US-10-001-876-8	Sequence 8, Appl	c 334	38	1.0	2292	9	US-10-198-846-10658	Sequence 10658, A
262	38	1.0	625	9	US-10-198-846-8846	Sequence 8846, Ap	c 335	38	1.0	2409	10	US-09-839-497A-8	Sequence 8, Appl
263	38	1.0	637	9	US-10-016-634A-83	Sequence 83, Appl	336	38	1.0	2507	12	US-10-044-090-783	Sequence 783, App
264	38	1.0	654	9	US-10-001-876-103	Sequence 103, App	337	38	1.0	2644	10	US-09-833-381-868	Sequence 868, App
265	38	1.0	664	9	US-10-198-846-8060	Sequence 8060, Ap	338	38	1.0	2832	10	US-09-764-864-371	Sequence 371, App
266	38	1.0	664	9	US-10-198-846-8060	Sequence 8060, Ap	c 339	38	1.0	3075	10	US-09-833-381-1947	Sequence 1947, Ap
267	38	1.0	665	9	US-10-198-846-1717	Sequence 1717, Ap	340	38	1.0	3110	9	US-10-198-846-9938	Sequence 9938, Ap
268	38	1.0	667	9	US-10-002-344A-103	Sequence 103, App	341	38	1.0	3207	9	US-10-071-766-88	Sequence 88, Appl
269	38	1.0	687	10	US-09-962-436-41	Sequence 41, Appl	c 342	38	1.0	3337	9	US-10-198-846-10985	Sequence 10985, A
270	38	1.0	708	10	US-09-833-381-1258	Sequence 1258, Ap	c 343	38	1.0	3607	9	US-09-981-353-155	Sequence 155, App
271	38	1.0	727	12	US-10-001-879-84	Sequence 84, Appl	c 344	38	1.0	4021	9	US-10-071-766-57	Sequence 57, Appl
272	38	1.0	734	10	US-09-995-494-13	Sequence 13, Appl	c 345	38	1.0	4021	12	US-10-002-600-40	Sequence 40, Appl
273	38	1.0	780	9	US-09-867-915-27	Sequence 27, Appl	c 346	38	1.0	4395	9	US-10-198-846-13574	Sequence 13574, A
274	38	1.0	780	9	US-09-867-915-27	Sequence 27, Appl	c 347	38	1.0	4467	10	US-09-349-015-21	Sequence 21, Appl
275	38	1.0	781	10	US-09-910-943-383	Sequence 383, App	c 348	38	1.0	4563	12	US-10-002-600-26	Sequence 26, Appl
276	38	1.0	790	9	US-10-198-846-12288	Sequence 12288, A	349	38	1.0	4576	12	US-10-044-090-703	Sequence 703, App
277	38	1.0	792	9	US-10-198-846-4417	Sequence 4417, Ap	c 350	38	1.0	4712	9	US-09-974-298-180	Sequence 180, App
278	38	1.0	800	12	US-10-001-879-64	Sequence 64, Appl	c 351	38	1.0	5394	9	US-10-071-766-74	Sequence 74, Appl
279	38	1.0	801	9	US-10-082-830-92	Sequence 92, Appl	352	38	1.0	5464	10	US-09-741-153-3	Sequence 3, Appl
280	38	1.0	805	9	US-09-989-920-41	Sequence 41, Appl	c 353	38	1.0	5464	10	US-09-741-153-3	Sequence 3, Appl
281	38	1.0	813	9	US-10-198-846-9643	Sequence 9643, Ap	c 354	38	1.0	6615	9	US-10-029-413A-9	Sequence 9, Appl
282	38	1.0	825	9	US-10-198-846-9241	Sequence 9241, Ap	355	38	1.0	7819	10	US-09-955-866-14	Sequence 14, Appl
283	38	1.0	829	9	US-10-198-846-5328	Sequence 5328, Ap	c 356	38	1.0	7819	10	US-09-955-866-14	Sequence 14, Appl
284	38	1.0	830	9	US-10-198-846-3049	Sequence 3049, Ap	c 357	38	1.0	8674	12	US-10-044-090-814	Sequence 814, App
285	38	1.0	833	9	US-10-198-846-9070	Sequence 9070, Ap	358	38	1.0	8925	9	US-09-802-640-27	Sequence 27, Appl
286	38	1.0	847	9	US-10-198-846-3295	Sequence 3295, Ap	359	38	1.0	9179	10	US-09-955-866-16	Sequence 16, Appl
287	38	1.0	848	9	US-10-198-846-5016	Sequence 5016, Ap	c 360	38	1.0	9179	10	US-09-955-866-16	Sequence 16, Appl
288	38	1.0	855	9	US-10-198-846-13201	Sequence 13201, A	c 361	38	1.0	13182	10	US-09-817-199A-3	Sequence 3, Appl
289	38	1.0	857	9	US-10-198-846-5325	Sequence 5325, Ap	362	38	1.0	1752	10	US-09-748-127-3	Sequence 3, Appl
290	38	1.0	858	9	US-10-198-846-3300	Sequence 3300, Ap	c 363	38	1.0	19806	9	US-10-118-037-3	Sequence 3, Appl
291	38	1.0	860	9	US-10-198-846-6112	Sequence 6112, Ap	c 364	38	1.0	21784	10	US-09-820-002-3	Sequence 3, Appl
292	38	1.0	869	9	US-10-198-846-6262	Sequence 6262, Ap	c 365	38	1.0	21990	9	US-09-942-429A-9	Sequence 9, Appl
293	38	1.0	871	9	US-10-198-846-3735	Sequence 3735, Ap	c 366	38	1.0	31766	9	US-10-288-478-5	Sequence 5, Appl
294	38	1.0	875	9	US-10-198-846-4245	Sequence 4245, Ap	c 367	38	1.0	31766	10	US-09-765-344-5	Sequence 5, Appl
295	38	1.0	879	9	US-10-198-846-6634	Sequence 6634, Ap	368	38	1.0	31814	10	US-09-817-182-3	Sequence 3, Appl
296	38	1.0	883	9	US-10-198-846-6966	Sequence 6966, Ap	c 369	38	1.0	31814	10	US-09-817-182-3	Sequence 3, Appl
297	38	1.0	886	9	US-10-198-846-3058	Sequence 3058, Ap	c 370	38	1.0	34337	10	US-09-741-149-3	Sequence 3, Appl
298	38	1.0	899	9	US-10-198-846-12466	Sequence 12466, A	c 371	38	1.0	45862	9	US-10-216-355-3	Sequence 3, Appl
299	38	1.0	909	9	US-10-198-846-2884	Sequence 2884, Ap	c 372	38	1.0	46050	10	US-09-820-003A-3	Sequence 3, Appl
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303	38	1.0	962	9	US-10-198-846-10845	Sequence 10845, A	c 376	38	1.0	65042	9	US-10-229-124-3	Sequence 3, Appl
304	38	1.0	999	9	US-10-103-200A-17	Sequence 17, Appl	c 377	38	1.0	65042	9	US-10-229-124-3	Sequence 3, Appl
305	38	1.0	1024	9	US-10-202-193-49	Sequence 49, Appl	378	38	1.0	65464	9	US-09-859-888-3	Sequence 3, Appl
306	38	1.0	1033	9	US-10-002-344A-53	Sequence 53, Appl	c 379	38	1.0	69327	10	US-09-777-921A-3	Sequence 3, Appl
307	38	1.0	1035	9	US-10-002-344A-85	Sequence 85, Appl	c 380	38	1.0	74962	9	US-10-274-974-3	Sequence 3, Appl
308	38	1.0	1061	9	US-10-198-846-6965	Sequence 6965, Ap	381	38	1.0	83450	9	US-09-811-469-3	Sequence 3, Appl
309	38	1.0	1109	10	US-09-349-015-19	Sequence 19, Appl	382	38	1.0	148567	9	US-10-254-869-3	Sequence 3, Appl
310	38	1.0	1118	9	US-10-198-846-5504	Sequence 5504, Ap	383	38	1.0	148567	9	US-09-801-876B-3	Sequence 3, Appl
311	38	1.0	1134	9	US-10-002-344A-42	Sequence 42, Appl	384	38	1.0	170834	10	US-09-835-232-7	Sequence 7, Appl

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386	38	1.0	174493	9	US-10-238-709-3	Sequence 3, Appli	c 459	37	1.0	80	9	US-10-172-620-8	Sequence 8, Appli
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388	38	1.0	174493	10	US-09-804-471A-3	Sequence 3, Appli	461	37	1.0	81	9	US-09-860-474-60	Sequence 60, Appli
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392	38	1.0	197997	9	US-09-822-246-3	Sequence 3, Appli	c 465	37	1.0	81	9	US-10-223-126-72	Sequence 72, Appli
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c 448	37	1.0	72	9	US-10-223-126-63	Sequence 63, Appli	c 521	37	1.0	115	9	US-10-223-126-106	Sequence 106, Appli
c 449	37	1.0	73	9	US-10-223-126-64	Sequence 64, Appli	c 522	37	1.0	115	9	US-10-223-126-107	Sequence 107, Appli
c 450	37	1.0	74	9	US-09-201-396-18	Sequence 18, Appli	c 523	37	1.0	117	9	US-10-223-126-108	Sequence 108, Appli
c 451	37	1.0	74	9	US-10-223-126-65	Sequence 65, Appli	c 524	37	1.0	118	9	US-10-223-126-109	Sequence 109, Appli
c 452	37	1.0	75	9	US-10-223-126-66	Sequence 66, Appli	c 525	37	1.0	119	9	US-10-223-126-110	Sequence 110, Appli
c 453	37	1.0	76	9	US-10-223-126-67	Sequence 67, Appli	c 526	37	1.0	120	9	US-10-223-126-111	Sequence 111, Appli
c 454	37	1.0	76	10	US-09-815-171A-6	Sequence 6, Appli	c 527	37	1.0	121	9	US-10-108-077-10	Sequence 10, Appli
c 455	37	1.0	77	9	US-10-223-126-68	Sequence 68, Appli	c 528	37	1.0	121	9	US-10-223-126-112	Sequence 112, Appli
c 456	37	1.0	78	9	US-10-223-126-69	Sequence 69, Appli	c 529	37	1.0	121	10	US-09-867-262-9	Sequence 9, Appli
c 457	37	1.0	79	9	US-10-223-126-70	Sequence 70, Appli	c 530	37	1.0	121	10	US-09-885-551A-10	Sequence 10, Appli

C 531	37	1.0	121	12	US-10-087-426-10	Sequence 10, Appl	604	37	1.0	297	9	US-10-043-487-66	Sequence 66, Appl
C 532	37	1.0	122	9	US-10-223-126-113	Sequence 113, App	C 605	37	1.0	299	9	US-10-043-487-94	Sequence 94, Appl
C 533	37	1.0	123	9	US-10-108-077-9	Sequence 9, Appl	606	37	1.0	300	10	US-09-234-093B-5686	Sequence 5686, Ap
C 534	37	1.0	123	9	US-10-223-126-114	Sequence 114, App	607	37	1.0	317	10	US-09-294-093B-5547	Sequence 5547, Ap
C 535	37	1.0	123	10	US-09-867-262-8	Sequence 8, Appl	608	37	1.0	326	10	US-09-878-574-4464	Sequence 4464, Ap
C 536	37	1.0	123	10	US-09-885-551A-9	Sequence 9, Appl	C 609	37	1.0	326	10	US-09-878-574-4464	Sequence 4464, Ap
C 537	37	1.0	123	12	US-10-087-426-9	Sequence 9, Appl	C 610	37	1.0	328	9	US-10-082-830-132	Sequence 132, App
C 538	37	1.0	124	9	US-10-223-126-115	Sequence 115, App	C 611	37	1.0	344	9	US-10-001-857-10	Sequence 10, Appl
C 539	37	1.0	125	9	US-10-223-126-116	Sequence 116, App	612	37	1.0	345	9	US-09-995-025-16	Sequence 16, Appl
C 540	37	1.0	126	9	US-10-223-126-117	Sequence 117, App	613	37	1.0	345	9	US-09-995-040-16	Sequence 16, Appl
C 541	37	1.0	127	9	US-10-223-126-118	Sequence 118, App	614	37	1.0	345	9	US-09-998-817-16	Sequence 16, Appl
C 542	37	1.0	128	9	US-10-223-126-119	Sequence 119, App	615	37	1.0	345	9	US-09-998-817-16	Sequence 16, Appl
C 543	37	1.0	129	9	US-10-223-126-120	Sequence 120, App	616	37	1.0	345	9	US-10-040-937-16	Sequence 16, Appl
C 544	37	1.0	130	9	US-09-879-813-52	Sequence 52, Appl	C 617	37	1.0	345	9	US-09-918-995-29865	Sequence 29865, A
C 545	37	1.0	130	9	US-09-879-813-52	Sequence 52, Appl	618	37	1.0	353	9	US-10-000-256A-80	Sequence 80, Appl
C 546	37	1.0	131	9	US-10-223-126-121	Sequence 121, App	C 619	37	1.0	360	9	US-10-002-344A-55	Sequence 55, Appl
C 547	37	1.0	131	9	US-10-223-126-122	Sequence 122, App	C 620	37	1.0	360	9	US-09-918-995-7501	Sequence 7501, Ap
C 548	37	1.0	132	9	US-10-223-126-123	Sequence 123, App	621	37	1.0	373	9	US-10-016-157A-122	Sequence 122, App
C 549	37	1.0	133	9	US-10-223-126-124	Sequence 124, App	C 622	37	1.0	374	9	US-09-918-995-33771	Sequence 33771, A
C 550	37	1.0	134	9	US-10-223-126-125	Sequence 125, App	C 623	37	1.0	390	9	US-10-016-157A-131	Sequence 131, App
C 551	37	1.0	135	9	US-10-223-126-126	Sequence 126, App	624	37	1.0	390	9	US-10-082-830-10	Sequence 10, Appl
C 552	37	1.0	136	9	US-10-223-126-127	Sequence 127, App	C 625	37	1.0	390	10	US-09-872-153-7	Sequence 7, Appl
C 553	37	1.0	137	9	US-10-223-126-128	Sequence 128, App	C 626	37	1.0	401	9	US-09-918-995-4092	Sequence 4092, Ap
C 554	37	1.0	138	9	US-10-223-126-129	Sequence 129, App	627	37	1.0	403	9	US-10-198-846-6128	Sequence 6128, Ap
C 555	37	1.0	139	9	US-10-223-126-130	Sequence 130, App	C 628	37	1.0	406	9	US-09-918-995-16807	Sequence 16807, A
C 556	37	1.0	140	9	US-10-223-126-131	Sequence 131, App	C 629	37	1.0	407	9	US-09-918-995-14312	Sequence 14312, A
C 557	37	1.0	141	9	US-10-223-126-132	Sequence 132, App	C 630	37	1.0	408	12	US-10-001-879-48	Sequence 48, Appl
C 558	37	1.0	142	9	US-10-223-126-133	Sequence 133, App	631	37	1.0	416	9	US-10-198-846-9365	Sequence 9365, Ap
C 559	37	1.0	143	9	US-10-223-126-134	Sequence 134, App	C 632	37	1.0	422	9	US-10-198-846-3252	Sequence 3252, Ap
C 560	37	1.0	144	9	US-10-223-126-135	Sequence 135, App	C 633	37	1.0	422	10	US-09-833-381-239	Sequence 239, App
C 561	37	1.0	145	9	US-10-223-126-136	Sequence 136, App	C 634	37	1.0	424	9	US-09-918-995-35911	Sequence 35911, A
C 562	37	1.0	146	9	US-10-223-126-137	Sequence 137, App	C 635	37	1.0	430	9	US-10-016-634A-67	Sequence 67, Appl
C 563	37	1.0	147	9	US-10-223-126-138	Sequence 138, App	C 636	37	1.0	430	9	US-10-016-634A-67	Sequence 67, Appl
C 564	37	1.0	147	9	US-10-223-126-139	Sequence 139, App	C 637	37	1.0	440	9	US-10-000-256A-114	Sequence 114, App
C 565	37	1.0	149	9	US-10-223-126-140	Sequence 140, App	C 638	37	1.0	441	9	US-10-198-846-4895	Sequence 4895, Ap
C 566	37	1.0	150	9	US-10-223-126-141	Sequence 141, App	C 639	37	1.0	442	10	US-09-812-102-11	Sequence 11, Appl
C 567	37	1.0	151	9	US-10-223-126-142	Sequence 142, App	C 640	37	1.0	444	9	US-09-918-995-31562	Sequence 31562, A
C 568	37	1.0	152	9	US-10-223-126-143	Sequence 143, App	C 641	37	1.0	449	9	US-10-198-846-13613	Sequence 13613, A
C 569	37	1.0	153	9	US-10-223-126-144	Sequence 144, App	C 642	37	1.0	453	9	US-10-198-846-12821	Sequence 12821, A
C 570	37	1.0	154	9	US-09-884-566-7	Sequence 7, Appl	643	37	1.0	456	9	US-10-002-344A-106	Sequence 106, App
C 571	37	1.0	154	9	US-10-223-126-145	Sequence 145, App	C 644	37	1.0	461	9	US-09-918-995-20879	Sequence 20879, A
C 572	37	1.0	154	9	US-10-223-126-147	Sequence 147, App	C 645	37	1.0	464	9	US-10-198-846-12147	Sequence 12147, A
C 573	37	1.0	155	9	US-10-223-126-146	Sequence 146, App	646	37	1.0	465	9	US-10-071-766-75	Sequence 75, Appl
C 574	37	1.0	157	9	US-10-223-126-148	Sequence 148, App	C 647	37	1.0	466	9	US-10-198-846-9502	Sequence 9502, Ap
C 575	37	1.0	158	9	US-10-223-126-149	Sequence 149, App	C 648	37	1.0	470	9	US-09-918-995-12497	Sequence 12497, A
C 576	37	1.0	159	9	US-10-223-126-150	Sequence 150, App	649	37	1.0	471	9	US-09-918-995-15927	Sequence 15927, A
C 577	37	1.0	160	9	US-10-223-126-151	Sequence 151, App	C 650	37	1.0	473	9	US-09-918-995-24807	Sequence 24807, A
C 578	37	1.0	161	9	US-10-223-126-152	Sequence 152, App	C 651	37	1.0	475	9	US-09-918-995-32075	Sequence 32075, A
C 579	37	1.0	162	9	US-10-223-126-153	Sequence 153, App	C 652	37	1.0	476	10	US-09-833-381-493	Sequence 493, App
C 580	37	1.0	163	9	US-10-223-126-154	Sequence 154, App	653	37	1.0	477	9	US-09-918-995-13559	Sequence 13559, A
C 581	37	1.0	166	9	US-09-879-813-31	Sequence 31, Appl	654	37	1.0	477	9	US-09-918-995-19447	Sequence 19447, A
C 582	37	1.0	171	10	US-09-910-943-184	Sequence 184, App	655	37	1.0	480	10	US-09-771-209-35	Sequence 35, Appl
C 583	37	1.0	171	10	US-09-910-943-184	Sequence 184, App	656	37	1.0	481	9	US-09-918-995-20978	Sequence 20978, A
C 584	37	1.0	193	9	US-10-082-830-116	Sequence 116, App	657	37	1.0	488	9	US-10-078-090-45	Sequence 45, Appl
C 585	37	1.0	193	9	US-10-082-830-116	Sequence 116, App	C 658	37	1.0	488	9	US-10-007-280A-84	Sequence 84, Appl
C 586	37	1.0	195	9	US-10-253-007-64	Sequence 64, Appl	659	37	1.0	488	9	US-09-918-995-13632	Sequence 13632, A
C 587	37	1.0	215	9	US-10-108-077-8	Sequence 8, Appl	C 660	37	1.0	489	9	US-10-001-883-30	Sequence 30, Appl
C 588	37	1.0	215	10	US-09-867-262-7	Sequence 7, Appl	C 661	37	1.0	490	9	US-09-918-995-32519	Sequence 32519, A
C 589	37	1.0	215	10	US-09-885-551A-8	Sequence 8, Appl	C 662	37	1.0	491	9	US-09-918-995-22560	Sequence 22560, A
C 590	37	1.0	215	12	US-10-087-426-8	Sequence 8, Appl	663	37	1.0	492	9	US-09-918-995-2286	Sequence 2286, Ap
C 591	37	1.0	217	9	US-10-082-830-29	Sequence 29, Appl	664	37	1.0	492	9	US-09-918-995-5264	Sequence 5264, Ap
C 592	37	1.0	229	10	US-09-923-876-2247	Sequence 2247, Ap	C 665	37	1.0	492	9	US-09-918-995-19293	Sequence 19293, A
C 593	37	1.0	229	10	US-09-923-876-2247	Sequence 2247, Ap	C 666	37	1.0	492	9	US-09-918-995-19506	Sequence 19506, A
C 594	37	1.0	252	9	US-10-198-846-9990	Sequence 9990, Ap	C 667	37	1.0	493	9	US-09-736-457-13	Sequence 13, Appl
C 595	37	1.0	257	9	US-10-007-280A-25	Sequence 25, Appl	668	37	1.0	493	9	US-09-902-941-13	Sequence 13, Appl
C 596	37	1.0	258	9	US-10-198-846-10304	Sequence 10304, A	669	37	1.0	493	9	US-09-849-626-13	Sequence 13, Appl
C 597	37	1.0	258	12	US-10-006-773-7	Sequence 7, Appl	670	37	1.0	493	9	US-10-017-754-13	Sequence 13, Appl
C 598	37	1.0	268	10	US-09-848-889-4	Sequence 4, Appl	C 671	37	1.0	493	9	US-09-918-995-11006	Sequence 11006, A
C 599	37	1.0	268	10	US-09-848-889-4	Sequence 4, Appl	C 672	37	1.0	493	9	US-09-918-995-15639	Sequence 15639, A
C 600	37	1.0	270	10	US-09-923-876-4507	Sequence 4507, Ap	C 673	37	1.0	493	9	US-09-918-995-20998	Sequence 20998, A
C 601	37	1.0	289	10	US-09-234-093B-3157	Sequence 3157, Ap	C 674	37	1.0	493	9	US-10-198-846-9528	Sequence 9528, Ap
C 602	37	1.0	289	10	US-09-234-093B-3157	Sequence 3157, Ap	C 675	37	1.0	494	9	US-09-918-995-2820	Sequence 2820, Ap
C 603	37	1.0	291	10	US-09-833-381-140	Sequence 140, App	676	37	1.0	497	12	US-10-001-879-97	Sequence 97, Appl

c 677	1.0	500	9	US-09-918-995-10695	Sequence 10695, A	c 750	37	1.0	632	9	US-10-198-846-4836	Sequence 4836, Ap
c 678	1.0	506	9	US-09-918-995-12167	Sequence 12167, A	751	37	1.0	634	9	US-10-198-846-4831	Sequence 8831, Ap
c 679	1.0	506	9	US-09-918-995-19851	Sequence 19851, A	c 752	37	1.0	634	9	US-10-198-846-4831	Sequence 8831, Ap
c 680	1.0	507	9	US-09-918-995-20255	Sequence 20255, A	c 753	37	1.0	635	9	US-10-198-846-4868	Sequence 8868, Ap
c 681	1.0	515	9	US-10-007-280A-42	Sequence 42, Appl	754	37	1.0	635	9	US-10-198-846-4868	Sequence 8868, Ap
c 682	1.0	515	9	US-09-918-995-30655	Sequence 30655, A	c 755	37	1.0	635	9	US-10-198-846-4868	Sequence 8868, Ap
c 683	1.0	515	9	US-09-918-995-30655	Sequence 30655, A	756	37	1.0	635	9	US-10-198-846-4868	Sequence 8868, Ap
c 684	1.0	515	9	US-10-198-846-8481	Sequence 8481, Ap	c 757	37	1.0	637	9	US-10-016-634A-83	Sequence 83, Appl
c 685	1.0	515	9	US-10-198-846-9239	Sequence 9239, Ap	758	37	1.0	639	9	US-10-198-846-9050	Sequence 9050, Ap
c 686	1.0	524	10	US-09-833-381-492	Sequence 492, Appl	759	37	1.0	639	10	US-09-880-107-3484	Sequence 3484, Ap
c 687	1.0	526	10	US-09-954-436-1885	Sequence 1885, Ap	c 760	37	1.0	641	9	US-10-198-846-6063	Sequence 6063, Ap
c 688	1.0	527	9	US-10-000-256A-52	Sequence 52, Appl	c 761	37	1.0	641	9	US-10-198-846-6063	Sequence 6063, Ap
c 689	1.0	529	9	US-10-002-344A-79	Sequence 79, Appl	c 762	37	1.0	641	9	US-10-198-846-6063	Sequence 6063, Ap
c 690	1.0	530	9	US-09-989-920-44	Sequence 44, Appl	c 763	37	1.0	642	9	US-10-198-846-6063	Sequence 6063, Ap
c 691	1.0	530	9	US-10-007-280A-43	Sequence 43, Appl	c 764	37	1.0	642	9	US-10-198-846-6063	Sequence 6063, Ap
c 692	1.0	531	9	US-10-198-846-9095	Sequence 9095, Ap	765	37	1.0	643	9	US-10-198-846-6061	Sequence 6061, Ap
c 693	1.0	532	9	US-10-198-846-13798	Sequence 13798, A	c 766	37	1.0	646	10	US-09-771-209-23	Sequence 23, Appl
c 694	1.0	535	9	US-09-292-758-76	Sequence 76, Appl	c 767	37	1.0	646	10	US-09-771-209-23	Sequence 23, Appl
c 695	1.0	537	9	US-10-000-256A-55	Sequence 55, Appl	c 768	37	1.0	646	10	US-09-771-209-23	Sequence 23, Appl
c 696	1.0	537	9	US-09-918-995-28028	Sequence 28028, A	c 769	37	1.0	646	10	US-09-771-209-23	Sequence 23, Appl
c 697	1.0	544	10	US-09-757-781-45	Sequence 45, Appl	c 770	37	1.0	647	9	US-10-198-846-6061	Sequence 6061, Ap
c 698	1.0	548	9	US-10-016-157A-28	Sequence 28, Appl	c 771	37	1.0	647	9	US-10-198-846-6061	Sequence 6061, Ap
c 699	1.0	549	9	US-09-918-995-16128	Sequence 16128, A	c 772	37	1.0	648	9	US-10-198-846-6061	Sequence 6061, Ap
c 700	1.0	550	9	US-10-198-846-13099	Sequence 13099, A	c 773	37	1.0	650	9	US-10-198-846-6060	Sequence 6060, Ap
c 701	1.0	552	9	US-09-918-995-12506	Sequence 12506, A	c 774	37	1.0	650	9	US-10-198-846-6060	Sequence 6060, Ap
c 702	1.0	554	9	US-10-074-475-60	Sequence 60, Appl	c 775	37	1.0	651	9	US-10-198-846-6061	Sequence 6061, Ap
c 703	1.0	557	12	US-10-001-843-4	Sequence 4, Appl	c 776	37	1.0	651	9	US-10-198-846-6061	Sequence 6061, Ap
c 704	1.0	562	9	US-10-011-585A-125	Sequence 125, Appl	c 777	37	1.0	655	9	US-10-198-846-6061	Sequence 6061, Ap
c 705	1.0	562	9	US-09-918-995-12370	Sequence 12370, A	c 778	37	1.0	655	10	US-09-880-107-3489	Sequence 3489, Ap
c 706	1.0	565	9	US-10-198-846-10923	Sequence 10923, A	c 779	37	1.0	655	10	US-10-198-846-6061	Sequence 6061, Ap
c 707	1.0	566	9	US-10-198-846-12670	Sequence 12670, A	c 780	37	1.0	657	9	US-10-198-846-6061	Sequence 6061, Ap
c 708	1.0	569	9	US-09-918-995-15940	Sequence 15940, A	c 781	37	1.0	657	10	US-09-880-107-3487	Sequence 3487, Ap
c 709	1.0	572	9	US-10-007-280A-64	Sequence 64, Appl	c 782	37	1.0	657	10	US-09-880-107-3487	Sequence 3487, Ap
c 710	1.0	573	10	US-09-833-381-677	Sequence 67, Appl	c 783	37	1.0	661	10	US-09-880-107-3488	Sequence 3488, Ap
c 711	1.0	574	9	US-10-198-846-8326	Sequence 8326, Ap	c 784	37	1.0	661	10	US-09-880-107-3488	Sequence 3488, Ap
c 712	1.0	575	9	US-09-918-995-26554	Sequence 26554, A	c 785	37	1.0	663	9	US-10-198-846-9197	Sequence 9197, Ap
c 713	1.0	576	9	US-09-918-995-15389	Sequence 15389, A	c 786	37	1.0	664	9	US-10-000-256A-10	Sequence 10, Appl
c 714	1.0	576	9	US-10-198-846-9129	Sequence 9129, Ap	c 787	37	1.0	664	9	US-10-198-846-2402	Sequence 2402, Ap
c 715	1.0	580	10	US-09-833-381-676	Sequence 676, Appl	c 788	37	1.0	664	9	US-10-198-846-8856	Sequence 8856, Ap
c 716	1.0	585	9	US-10-082-830-38	Sequence 38, Appl	c 789	37	1.0	665	9	US-10-198-846-13821	Sequence 13821, A
c 717	1.0	587	9	US-09-918-995-15078	Sequence 15078, A	c 790	37	1.0	666	9	US-10-198-846-8497	Sequence 8497, Ap
c 718	1.0	590	10	US-09-880-107-3485	Sequence 3485, Ap	c 791	37	1.0	667	12	US-10-001-870-92	Sequence 92, Appl
c 719	1.0	592	9	US-10-198-846-8360	Sequence 8360, Ap	c 792	37	1.0	672	9	US-10-198-846-7865	Sequence 7865, Ap
c 720	1.0	592	9	US-10-198-846-8361	Sequence 8361, Ap	c 793	37	1.0	672	9	US-10-198-846-8818	Sequence 8818, Ap
c 721	1.0	592	10	US-09-765-231A-83	Sequence 9, Appl	c 794	37	1.0	672	9	US-10-198-846-9524	Sequence 9524, Ap
c 722	1.0	593	9	US-10-198-846-8741	Sequence 8741, Ap	c 795	37	1.0	675	9	US-10-198-846-8672	Sequence 8672, Ap
c 723	1.0	597	9	US-10-198-846-9361	Sequence 9361, Ap	c 796	37	1.0	678	9	US-10-198-846-12844	Sequence 12844, A
c 724	1.0	598	10	US-09-812-102-31	Sequence 31, Appl	c 797	37	1.0	679	9	US-10-198-846-3169	Sequence 3169, Ap
c 725	1.0	604	9	US-10-198-846-9019	Sequence 9019, Ap	c 798	37	1.0	684	9	US-10-198-846-2063	Sequence 2063, Ap
c 726	1.0	604	9	US-10-198-846-9019	Sequence 9019, Ap	c 799	37	1.0	688	9	US-10-080-980-8	Sequence 8, Appl
c 727	1.0	605	9	US-10-284-985-19	Sequence 19, Appl	c 800	37	1.0	695	9	US-10-016-157A-69	Sequence 69, Appl
c 728	1.0	605	9	US-10-284-985-19	Sequence 19, Appl	c 801	37	1.0	698	9	US-10-001-835-50	Sequence 50, Appl
c 729	1.0	606	9	US-10-034-934-9	Sequence 9, Appl	c 802	37	1.0	701	9	US-10-198-846-2832	Sequence 2832, Ap
c 730	1.0	611	9	US-10-198-846-8503	Sequence 8503, Ap	c 803	37	1.0	702	9	US-10-198-846-2127	Sequence 2127, Ap
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c 733	1.0	613	9	US-10-198-846-8743	Sequence 8743, Ap	c 806	37	1.0	704	9	US-10-198-846-3574	Sequence 3574, Ap
c 734	1.0	614	9	US-10-198-846-8324	Sequence 8324, Ap	c 807	37	1.0	706	9	US-10-198-846-8653	Sequence 8653, Ap
c 735	1.0	614	9	US-10-198-846-8324	Sequence 8324, Ap	c 808	37	1.0	707	9	US-10-198-846-8343	Sequence 8343, Ap
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; CURRENT APPLICATION NUMBER: US/09/840,989A
; CURRENT FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: PCT/US00/29432
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,740
; PRIOR FILING DATE: 1999-10-27
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3	AAAAAAAAAA	CCCCCAACAA	CTTAGCGGAA	ACTTCTCAGAGAA	TGCTC	CAAAA	ACTCAGCA	62
192	GTGCTTCT	TGCTGGT	GATCAGT	GCCTTCTGCA	ACCCATCAG	CGGGAGCAG	AATGACTCT	251
63	GTGCTTCT	TGCTGGT	GATCAGT	GCCTTCTGCA	ACCCATCAG	CGGGAGCAG	AATGACTCT	122
252	GTGACCCC	CAGAAATCC	CAGTGC	GCCTCAAA	AACTCAGTGA	TGGTTCG	TCCCTC	311
123	GTGACCCC	CAGAAATCC	CAGTGC	GCCTCAAA	AACTCAGTGA	TGGTTCG	TCCCTC	182
312	AACAGTGT	CTACAGGT	CGGTCGGT	CGGGGCCTTT	TGCATGCTGC	TGGAAAA	ACTCCACTGTGAC	371

RESULT 5

```

US-10-116-051-1
; Sequence 1, Application US/10116051
; Patent No. US20020146791A1
; GENERAL INFORMATION:
; APPLICANT: Olsen et al.
; TITLE OF INVENTION: CORPUSCLES OF STANNIUS PROTEIN, STANNIOCALCIN
; FILE REFERENCE: PF108P1D1C1
; CURRENT APPLICATION NUMBER: US/10/116,051
; CURRENT FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 09/312,610
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 08/431,117
; PRIOR FILING DATE: 1995-04-28
; PRIOR APPLICATION NUMBER: 08/208,005
; PRIOR FILING DATE: 1994-03-08
; NUMBER OF SEQ ID NOS: 10

```

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 1

; LENGTH: 771

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-116-051-1

Query Match 19.1%; Score 720; DB 12; Length 771;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 770; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 159 GAACTTCTCAGAGATGCTCCAAACTCAGAGTGTCTTCTGCTGTGATCAGTGT 218
Db 1 GAACTTCTCAGAGATGCTCCAAACTCAGAGTGTCTTCTGCTGTGATCAGTGT 60
QY 219 TCTGCAACCCATGAGCGGAGCAGAGTACTCTGTAGCCGCCAGGAAATCCCGAGTGGG 278
Db 61 TCTGCAACCCATGAGCGGAGCAGAGTACTCTGTAGCCGCCAGGAAATCCCGAGTGGG 120
QY 279 GTCAAAATCAGCTGAAGTGTTCGTTGCCCTCAACAGTGTCTACAGTGGCTGCGGG 338
Db 121 GCCAAAATCAGCTGAAGTGTTCGTTGCCCTCAACAGTGTCTACAGTGGCTGCGGG 180
QY 339 GCTTTTGCATGCTCGAAACTCCACCTGTGACACAGATGGATGTATGACATCTGTAA 398
Db 181 GCTTTTGCATGCTCGAAACTCCACCTGTGACACAGATGGATGTATGACATCTGTAA 240
QY 399 TCCCTTCTGTACAGGCTGCTTAAATTTGACACTCAGGGAAGACATTCGTCAAAGAGC 458
Db 241 TCCCTTCTGTACAGGCTGCTTAAATTTGACACTCAGGGAAGACATTCGTCAAAGAGC 300
QY 459 TTTAAATGCATCGCCAAACGGGTCACTCCAAAGGTCTTCTGCCATTCGGAGTGTCT 518
Db 301 TTTAAATGCATCGCCAAACGGGTCACTCCAAAGGTCTTCTGCCATTCGGAGTGTCT 360
QY 519 ACTTTTCAAAGATGATTCCTGAGTGCAGGAAGTGTCTACAGAGCTGAATGTGTGC 578
Db 361 ACTTTTCAAAGATGATTCCTGAGTGCAGGAAGTGTCTACAGAGCTGAATGTGTGC 420
QY 579 AGCATCGCCAAAGCGAAACCTCAAGCCATCACTGAGGTGCTCGCCCAATCACTTC 638
Db 421 AGCATCGCCAAAGCGAAACCTCAAGCCATCACTGAGGTGCTCGCCCAATCACTTC 480
QY 639 TCCACAGATACTATAACAGACTTGTCCGAAGCTCTGGAATGTGATGAACACAGTC 698
Db 481 TCCACAGATACTATAACAGACTTGTCCGAAGCTCTGGAATGTGATGAACACAGTC 540
QY 699 AGCAATCAGACAGACCTGATGAGAAATTTGGCCCTTAACATGCCAGCCTCTCCAC 758
Db 541 AGCAATCAGACAGACCTGATGAGAAATTTGGCCCTTAACATGCCAGCCTCTCCAC 600
QY 759 ATCTTGCAGACAGACCTGTCCCAACACACACCCAGAGTGTCTCAACAGGAGCGC 818
Db 601 ATCTTGCAGACAGACCTGTCCCAACACACACCCAGAGTGTCTCAACAGGAGCGC 660
QY 819 ACCAATGAGCCGAGAGCTGAAAGTCTCTCCTCAGGAACTCCGAGGTGAGGAGCTCT 878
Db 661 ACCAATGAGCCGAGAGCTGAAAGTCTCTCCTCAGGAACTCCGAGGTGAGGAGCTCT 720
QY 879 CCTTCCCATCAACAGCAGATCCCATGAGTGTGATCAACAGGAGAGGT 929
Db 721 CCTTCCCATCAACAGCAGATCCCATGAGTGTGATCAACAGGAGAGGT 771
```

RESULT 6

US-09-778-320-149

; Sequence 149, Application US/09778320

; Patent No. US20010034052A1

; GENERAL INFORMATION:

; APPLICANT: Dillon, Davin C.

; APPLICANT: Day, Craig H.

; APPLICANT: Jiang, Yugu

; APPLICANT: Houghton, Raymond L.

; APPLICANT: Mitcham, Jennifer

; APPLICANT: Wang, Tongtong

; APPLICANT: McNeill, Patricia D.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; FILE REFERENCE: 210121.491C5

; CURRENT APPLICATION NUMBER: US/09/778.320

; CURRENT FILING DATE: 2001-02-06

; NUMBER OF SEQ ID NOS: 301

; SOFTWARE: Fast-Seq for Windows Version 3.0

; SEQ ID NO 149

; LENGTH: 585

; TYPE: DNA

; ORGANISM: Homo sapiens

; NAME/KEY: misc feature

; LOCATION: (1)-(585)

; OTHER INFORMATION: n=A,T,C or G

US-09-778-320-149

Query Match

Best Local Similarity 100.0%; Pred. No. 8.3e-241; Length 585;

Matches 494; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 435 GGAAGAAGATTCGTCAAAGAGAGCTTAAATGTCATCGCCAAACGGGGTCACTTCCAGGTC 494
Db 33 GGAAGAAGATTCGTCAAAGAGAGCTTAAATGTCATCGCCAAACGGGGTCACTTCCAGGTC 92
QY 495 TTCTTCGCCATTCGGAGGTGCTCCACTTTCCAAAGGATGATTGCTGAGGTGCGAGAGAG 554
Db 93 TTCTTCGCCATTCGGAGGTGCTCCACTTTCCAAAGGATGATTGCTGAGGTGCGAGAGAG 152
QY 555 TGCTACAGCAAGCTGAATGTGTGAGCATCGCCAAAGCGGAACCTTGAAGCCATCACTGAG 614
Db 153 TGCTACAGCAAGCTGAATGTGTGAGCATCGCCAAAGCGGAACCTTGAAGCCATCACTGAG 212
QY 615 GTCGTCCAGTGCCTCAATCACTTTTCCAAAGATATAACAGACTTTGTCCGAAGCCTG 674
Db 213 GTCGTCCAGTGCCTCAATCACTTTTCCAAAGATATAACAGACTTTGTCCGAAGCCTG 272
QY 675 CTGGAATGTGATGAGACACAGTGTGAGCATCAAGACAGCCCTGATGGAGAAATTTGG 734
Db 273 CTGGAATGTGATGAGACACAGTGTGAGCATCAAGACAGCCCTGATGGAGAAATTTGG 332
QY 735 CCTAACATGGCCAGCTCTTCCACATCTGTGAGACAGACCACTGTGCCCAACACACCCA 794
Db 333 CCTAACATGGCCAGCTCTTCCACATCTGTGAGACAGACCACTGTGCCCAACACACCCA 392
QY 795 CGAGTGTACTTCAACAGGAGACGCAACCAATGAGCGCGAGAGCTGAAAGTCTCTCCTCAGG 854
Db 393 CGAGTGTACTTCAACAGGAGACGCAACCAATGAGCGCGAGAGCTGAAAGTCTCTCCTCAGG 452
QY 855 AACCTCCAGGTGAGGAGTCTTCCCTCCACATCAACAGCAGATCCCATGAGAGTGA 914
Db 453 AACCTCCAGGTGAGGAGTCTTCCCTCCACATCAACAGCAGATCCCATGAGAGTGA 512
QY 915 TAACCCAGGAGAGG 928
Db 513 TAACCCAGGAGAGG 526
```

RESULT 7

US-09-910-689-149

; Sequence 149, Application US/09910689

; Patent No. US20020081609A1

; GENERAL INFORMATION:

; APPLICANT: Dillon, Davin C.

; APPLICANT: Day, Craig H.

; APPLICANT: Jiang, Yugu

; APPLICANT: Houghton, Raymond L.

; APPLICANT: Mitcham, Jennifer

; APPLICANT: Wang, Tongtong

; APPLICANT: McNeill, Patricia D.

; APPLICANT: Harlocker, Susan L.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 ; FILE REFERENCE: 210121.491C6
 ; CURRENT APPLICATION NUMBER: US/09/910,689
 ; CURRENT FILING DATE: 2001-07-20
 ; NUMBER OF SEQ ID NOS: 307
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 149
 ; LENGTH: 585
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; NAME/KEY: misc feature
 ; LOCATION: 10, 30, 32, 527, 565
 ; OTHER INFORMATION: n = A,T,C or G
 US-09-910-689-149

Query Match 13.1%; Score 494; DB 10; Length 585;
 Best Local Similarity 100.0%; Pred. No. 8.3e-241;
 Matches 494; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 435 GGAAGAAGCATTCGTCAAGAGAGCTTAAATGATCGCCAAACGGGGTCACTCCCAAGGTC 494
 Db 33 GGAAGAAGCATTCGTCAAGAGAGCTTAAATGATCGCCAAACGGGGTCACTCCCAAGGTC 92
 QY 495 TTCTCTCGCCATTCGGAGGTCCTCCACTTTCCAAAGGATGATTGCTGAGGTGAGGAAGAG 554
 Db 93 TTCTCTCGCCATTCGGAGGTCCTCCACTTTCCAAAGGATGATTGCTGAGGTGAGGAAGAG 152
 QY 555 TGCTACAGCAAGCTGAATGTGTGAGCATCGCCAAAGCGGAACCCCTGAAGCCATCACTGAG 614
 Db 153 TGCTACAGCAAGCTGAATGTGTGAGCATCGCCAAAGCGGAACCCCTGAAGCCATCACTGAG 212
 QY 615 GTCTGTCAGCTGCCCAATCACTTTCCAAACAGACTATAAAGAGCTTGTCCGAAGCCTG 674
 Db 213 GTCTGTCAGCTGCCCAATCACTTTCCAAACAGACTATAAAGAGCTTGTCCGAAGCCTG 272
 QY 675 CTGGAATGTGATGAAGACACAGTCAGCAACATCAGAGACAGCTGATGAGAAAAATTGGG 734
 Db 273 CTGGAATGTGATGAAGACACAGTCAGCAACATCAGAGACAGCTGATGAGAAAAATTGGG 332
 QY 735 CCTAATATGCGCAGCTCTTCCACATCTCTGAGACAGACCACTGTGCCCAACACACCCA 794
 Db 333 CCTAATATGCGCAGCTCTTCCACATCTCTGAGACAGACCACTGTGCCCAACACACCCA 392
 QY 795 CGAGCTGACTTCAACAGGAGAGCCCAATGAGCCGAGAAAGCTGAAAGTCTCTCTCAGG 854
 Db 393 CGAGCTGACTTCAACAGGAGAGCCCAATGAGCCGAGAAAGCTGAAAGTCTCTCTCAGG 452
 QY 855 AACCTCCGAGGTGAGGAGGACTCTCCCTCCACATCAACAGCAGACATCCCATGAGAGTGA 914
 Db 453 AACCTCCGAGGTGAGGAGGACTCTCCCTCCACATCAACAGCAGACATCCCATGAGAGTGA 512
 QY 915 TAACCCAGGGAGAGG 928
 Db 513 TAACCCAGGGAGAGG 526

RESULT 8
 US-10-010-742-149
 ; Sequence 149, Application US/10010742
 ; Patent No. US2002014672A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dillon, Davin C.
 ; APPLICANT: Day, Craig H.
 ; APPLICANT: Jiang, Yuqiu
 ; APPLICANT: Houghton, Raymond L.
 ; APPLICANT: Mitcham, Jennifer L.
 ; APPLICANT: Wang, Tonglong
 ; APPLICANT: McNeill, Patricia D.
 ; APPLICANT: Harlocker, Susan L.
 ; APPLICANT: Bennington, Angela Ann

; APPLICANT: Zehentner, Barbara
 ; APPLICANT: Fanger, Gary R.
 ; APPLICANT: Reiter, Marc W.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 ; FILE REFERENCE: 210121.491C7
 ; CURRENT APPLICATION NUMBER: US/10/010,742
 ; CURRENT FILING DATE: 2001-11-30
 ; NUMBER OF SEQ ID NOS: 307
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 149
 ; LENGTH: 585
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; NAME/KEY: misc feature
 ; LOCATION: 10, 30, 32, 527, 565
 ; OTHER INFORMATION: n = A,T,C or G
 US-10-010-742-149

Query Match 13.1%; Score 494; DB 12; Length 585;
 Best Local Similarity 100.0%; Pred. No. 8.3e-241;
 Matches 494; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 435 GGAAGAAGCATTCGTCAAGAGAGCTTAAATGATCGCCAAACGGGGTCACTCCCAAGGTC 494
 Db 33 GGAAGAAGCATTCGTCAAGAGAGCTTAAATGATCGCCAAACGGGGTCACTCCCAAGGTC 92
 QY 495 TTCTCTCGCCATTCGGAGGTCCTCCACTTTCCAAAGGATGATTGCTGAGGTGAGGAAGAG 554
 Db 93 TTCTCTCGCCATTCGGAGGTCCTCCACTTTCCAAAGGATGATTGCTGAGGTGAGGAAGAG 152
 QY 555 TGCTACAGCAAGCTGAATGTGTGAGCATCGCCAAAGCGGAACCCCTGAAGCCATCACTGAG 614
 Db 153 TGCTACAGCAAGCTGAATGTGTGAGCATCGCCAAAGCGGAACCCCTGAAGCCATCACTGAG 212
 QY 615 GTCTGTCAGCTGCCCAATCACTTTCCAAACAGACTATAAAGAGCTTGTCCGAAGCCTG 674
 Db 213 GTCTGTCAGCTGCCCAATCACTTTCCAAACAGACTATAAAGAGCTTGTCCGAAGCCTG 272
 QY 675 CTGGAATGTGATGAAGACACAGTCAGCAACATCAGAGACAGCTGATGAGAAAAATTGGG 734
 Db 273 CTGGAATGTGATGAAGACACAGTCAGCAACATCAGAGACAGCTGATGAGAAAAATTGGG 332
 QY 735 CCTAATATGCGCAGCTCTTCCACATCTCTGAGACAGACCACTGTGCCCAACACACCCA 794
 Db 333 CCTAATATGCGCAGCTCTTCCACATCTCTGAGACAGACCACTGTGCCCAACACACCCA 392
 QY 795 CGAGCTGACTTCAACAGGAGAGCCCAATGAGCCGAGAAAGCTGAAAGTCTCTCTCAGG 854
 Db 393 CGAGCTGACTTCAACAGGAGAGCCCAATGAGCCGAGAAAGCTGAAAGTCTCTCTCAGG 452
 QY 855 AACCTCCGAGGTGAGGAGGACTCTCCCTCCACATCAACAGCAGACATCCCATGAGAGTGA 914
 Db 453 AACCTCCGAGGTGAGGAGGACTCTCCCTCCACATCAACAGCAGACATCCCATGAGAGTGA 512
 QY 915 TAACCCAGGGAGAGG 928
 Db 513 TAACCCAGGGAGAGG 526

RESULT 9
 US-10-060-036-2677/c
 ; Sequence 2677, Application US/10060036
 ; Publication No. US2003007314A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Benson, Darin R.
 ; APPLICANT: Kalos, Michael D.
 ; APPLICANT: Lodes, Michael J.
 ; APPLICANT: Persing, David H.
 ; APPLICANT: Hepler, William T.
 ; APPLICANT: Jiang, Yuqiu
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
; FILE REFERENCE: 210121.566
; CURRENT APPLICATION NUMBER: US/10/060,036
; CURRENT FILING DATE: 2002-01-30
; NUMBER OF SEQ ID NOS: 4560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2677
; LENGTH: 473
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-036-2677

Query Match 12.3%; Score 462; DB 9; Length 473;
Best Local Similarity 100.0%; Pred. No. 1.6e-224;
Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 518 CACTTTCCAAAGGATGATTGCTGAGGTGCGAGGAGAGTGCTACAGCAAGCTCAATGTGTG 577
DB 473 CACTTTCCAAAGATGATTGCTGAGGTGCGAGGAGAGTGCTACAGCAAGCTCAATGTGTG 414
QY 578 CAGCATCGCCAAAGCGGAACCTTGAAGCCATCACTGAGGTGCTCCAGCTGCCCAATCACTT 637
DB 413 CAGCATCGCCAAAGCGGAACCTTGAAGCCATCACTGAGGTGCTCCAGCTGCCCAATCACTT 354
QY 638 CTCCTCAACAGATCTATAACAGACTTGTCCGAAGCCTGTGGAATGTGATGAAGACACAGT 697
DB 353 CTCCTCAACAGATCTATAACAGACTTGTCCGAAGCCTGTGGAATGTGATGAAGACACAGT 294
QY 698 CAGCAATCAGACAGACGCTGATGAGAAATTTGGCCCTTAACATGCGCCAGCTCTTCCA 757
DB 293 CAGCAATCAGACAGACGCTGATGAGAAATTTGGCCCTTAACATGCGCCAGCTCTTCCA 234
QY 758 CATCTCTGACAGACGACCTGTGCCCAACACACACCCAGAGCTGACTTCAACAGAGAGCG 817
DB 233 CATCTCTGACAGACGACCTGTGCCCAACACACACCCAGAGCTGACTTCAACAGAGAGCG 174
QY 818 CACCAATGAGCGCAGAAAGTGAAGTCTCTCAGGAACCTCCAGAGTGAGGAGGACTC 877
DB 173 CACCAATGAGCGCAGAAAGTGAAGTCTCTCAGGAACCTCCAGAGTGAGGAGGACTC 114
QY 878 TCCTCTCCACATCAACGACACATCCATCAGAGTGATGATACCCAGGAGAGGTTATTCACA 937
DB 113 TCCTCTCCACATCAACGACACATCCATCAGAGTGATGATACCCAGGAGAGGTTATTCACA 54
QY 938 ACCTCACCACAACTAGTATCATTTAGGGGTGTTGACACACCA 979
DB 53 ACCTCACCACAACTAGTATCATTTAGGGGTGTTGACACACCA 12

RESULT 10
US-09-918-995-33032
; Sequence 33032, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 33032
; LENGTH: 436
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-995-33032

Query Match 11.6%; Score 436; DB 9; Length 436;
Best Local Similarity 100.0%; Pred. No. 2.8e-211;
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 686 TGAAGACACAGTCAGCAACAATCAGAGACAGCCTGATGAGAAAAATTTGGCCTTAACATGCG 745
DB 1 TGAAGACACAGTCAGCAACAATCAGAGACAGCCTGATGAGAAAAATTTGGCCTTAACATGCG 60
QY 746 CAGCCTCTTCCACATCTCTGCGAGACAGACCTGTGCCCAACACACACCCAGAGCTGACTT 805
DB 61 CAGCCTCTTCCACATCTCTGCGAGACAGACCTGTGCCCAACACACACCCAGAGCTGACTT 120
QY 806 CAACAGGAGAGCGCAATGAGCCGAGAGCTGAAAGTCTCTCTCAGGAACCTCCGAGG 865
DB 121 CAACAGGAGAGCGCAATGAGCCGAGAGCTGAAAGTCTCTCTCAGGAACCTCCGAGG 180
QY 866 TGAGGAGAGCTCTCCTCCCATCAATCAAAACGACATCCCATGAGAGTGATATAACAGGAG 925
DB 181 TGAGGAGAGCTCTCCTCCCATCAATCAAAACGACATCCCATGAGAGTGATATAACAGGAG 240
QY 926 AGTTTATTCACAACTCCACCAACTAGTATCATTTTAGGGGTGTTGACACACACCTTTG 985
DB 241 AGTTTATTCACAACTCCACCAACTAGTATCATTTTAGGGGTGTTGACACACACCTTTG 300
QY 986 AGTGTACTGTGCTGCTGTTGATTTTTTAAAGTAGTCTCTATTTTCTATCCCTTTAAAG 1045
DB 301 AGTGTACTGTGCTGCTGTTGATTTTTTAAAGTAGTCTCTATTTTCTATCCCTTTAAAG 360
QY 1046 AAAATTGCGATGAACCTAGGCTTCTGTAATCAATATCCCAACATTTGCAATGGCAGCAT 1105
DB 361 AAAATTGCGATGAACCTAGGCTTCTGTAATCAATATCCCAACATTTGCAATGGCAGCAT 420
QY 1106 CCCACCAACAAATCC 1121
DB 421 CCCACCAACAAATCC 436

RESULT 11
US-09-736-457-4/c
; Sequence 4, Application US/09736457
; Patent No. US20020168637A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedwick, Tom
; APPLICANT: Carter, Darriek
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; APPLICANT: Wang, Aijun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C15
; CURRENT APPLICATION NUMBER: US/09/736,457
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 1864
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 510
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-736-457-4

Query Match 10.8%; Score 405; DB 9; Length 510;
Best Local Similarity 100.0%; Pred. No. 1.8e-195;
Matches 405; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 TGTGGAATATAAATAGCTGAAAACTTAATGTACTGTACATAAATCCAGAGGACTCTGCTT 1703
DB 441 TGTGGAATATAAATAGCTGAAAACTTAATGTACTGTACATAAATCCAGAGGACTCTGCTT 382
QY 1704 AAACAAACAGTATATAAATCTTTATTCATATAGATTTAGTTTGTAACTTAGCTTTA 1763
DB 381 AAACAAACAGTATATAAATCTTTATTCATATAGATTTAGTTTGTAACTTAGCTTTA 322

QY 1764 TTTTCTTTTCTGGGAATGAATACTATCTCACTTCCAGATATCCACATATAATGCTCC 1823
DB 321 TTTTCTTTTCTGGGAATGAATACTATCTCACTTCCAGATATCCACATATAATGCTCC 262
QY 1824 TTGTGGCCCTTTTATAAATAAGGGGTAGAAGTAGTTTAAATTCACATCAAAACTTAA 1883
DB 261 TTGTGGCCCTTTTATAAATAAGGGGTAGAAGTAGTTTAAATTCACATCAAAACTTAA 202
QY 1884 GATGGCCCTGTATGACACAGGAATAACCAACAGGTTTATCTGAAGACCCAGGTAAGAT 1943
DB 201 GATGGCCCTGTATGACACAGGAATAACCAACAGGTTTATCTGAAGACCCAGGTAAGAT 142
QY 1944 GTTAATCTCCAGCCCACTCAACCCAGAGGCTACTCTTGACTTAGACCTATACTGAAAG 2003
DB 141 GTTAATCTCCAGCCCACTCAACCCAGAGGCTACTCTTGACTTAGACCTATACTGAAAG 82
QY 2004 ATCTCTGTGCATCCAACTGGAAATTCAGGAACCAAAAGAGCA 2048
DB 81 ATCTCTGTGCATCCAACTGGAAATTCAGGAACCAAAAGAGCA 37

RESULT 12

US-09-902-941-4/c

; Sequence 4, Application US/09902941

; Patent No. US20020172952A1

; GENERAL INFORMATION:

; APPLICANT: Henderson, Robert A.

; APPLICANT: Wang, Tonglong

; APPLICANT: Watanabe, Yoshihiro

; APPLICANT: Johnson, Jeffrey C.

; APPLICANT: Retter, Marc W.

; APPLICANT: Marnerakis, Margarita

; APPLICANT: Carter, Darrick

; APPLICANT: Fanger, Gary R.

; APPLICANT: Vedvick, Thomas S.

; APPLICANT: Bangur, Chaitanya S.

; APPLICANT: McNabb, Andria

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; FILE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

; FILE REFERENCE: 210121.478C17

; CURRENT APPLICATION NUMBER: US/09/902,941

; CURRENT FILING DATE: 2001-07-10

; NUMBER OF SEQ ID NOS: 2002

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 4

; LENGTH: 510

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-902-941-4

Query Match 10.8%; Score 405; DB 9; Length 510;

Best Local Similarity 100.0%; Pred. No. 1.8e-195;

Matches 405; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 TGTGGAATATAAATAGCTGAAACTAATCTACTGTACATAAATTCAGAGGACTCTGCTT 1703
DB 441 TGTGGAATATAAATAGCTGAAACTAATCTACTGTACATAAATTCAGAGGACTCTGCTT 382
QY 1704 AAACAAGCAGTATATAAATCTTTATTCATATAGATTTAGTTTGTAACTTAGCTTTA 1763
DB 381 AAACAAGCAGTATATAAATCTTTATTCATATAGATTTAGTTTGTAACTTAGCTTTA 322
QY 1764 TTTTCTTTTCTGGGAATGAATACTATCTCACTTCCAGATATCCACATATAATGCTCC 1823
DB 321 TTTTCTTTTCTGGGAATGAATACTATCTCACTTCCAGATATCCACATATAATGCTCC 262
QY 1824 TTGTGGCCCTTTTATAAATAAGGGGTAGAAGTAGTTTAAATTCACATCAAAACTTAA 1883
DB 261 TTGTGGCCCTTTTATAAATAAGGGGTAGAAGTAGTTTAAATTCACATCAAAACTTAA 202
QY 1884 GATGGCCCTGTATGACACAGGAATAACCAACAGGTTTATCTGAAGACCCAGGTAAGAT 1943

DB 201 GATGGCCCTGTATGACACAGGAATAACCAACAGGTTTATCTGAAGACCCAGGTAAGAT 142
QY 1944 GTTAATCTCCAGCCCACTCAACCCAGAGGCTACTCTTGACTTAGACCTATACTGAAAG 2003
DB 141 GTTAATCTCCAGCCCACTCAACCCAGAGGCTACTCTTGACTTAGACCTATACTGAAAG 82
QY 2004 ATCTCTGTGCATCCAACTGGAAATTCAGGAACCAAAAGAGCA 2048
DB 81 ATCTCTGTGCATCCAACTGGAAATTCAGGAACCAAAAGAGCA 37

RESULT 13

US-09-849-626-4/c

; Sequence 4, Application US/09849626

; Publication No. US20020197669A1

; GENERAL INFORMATION:

; APPLICANT: Bangur, Chaitanya

; APPLICANT: Fanger, Gary

; APPLICANT: Wang, Aijun

; APPLICANT: Wang, Tonglong

; APPLICANT: Switzer, Anne

; APPLICANT: McNeill, Patricia

; APPLICANT: Clapper, Jonathan

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; FILE OF INVENTION: DIAGNOSIS OF LUNG CANCER

; FILE REFERENCE: 210121.478C16

; CURRENT APPLICATION NUMBER: US/09/849,626

; CURRENT FILING DATE: 2001-05-03

; NUMBER OF SEQ ID NOS: 1926

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 4

; LENGTH: 510

; TYPE: DNA

; ORGANISM: Homo sapien

US-09-849-626-4

Query Match 10.8%; Score 405; DB 9; Length 510;

Best Local Similarity 100.0%; Pred. No. 1.8e-195;

Matches 405; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 TGTGGAATATAAATAGCTGAAACTAATCTACTGTACATAAATTCAGAGGACTCTGCTT 1703
DB 441 TGTGGAATATAAATAGCTGAAACTAATCTACTGTACATAAATTCAGAGGACTCTGCTT 382
QY 1704 AAACAAGCAGTATATAAATCTTTATTCATATAGATTTAGTTTGTAACTTAGCTTTA 1763
DB 381 AAACAAGCAGTATATAAATCTTTATTCATATAGATTTAGTTTGTAACTTAGCTTTA 322
QY 1764 TTTTCTTTTCTGGGAATGAATACTATCTCACTTCCAGATATCCACATATAATGCTCC 1823
DB 321 TTTTCTTTTCTGGGAATGAATACTATCTCACTTCCAGATATCCACATATAATGCTCC 262
QY 1824 TTGTGGCCCTTTTATAAATAAGGGGTAGAAGTAGTTTAAATTCACATCAAAACTTAA 1883
DB 261 TTGTGGCCCTTTTATAAATAAGGGGTAGAAGTAGTTTAAATTCACATCAAAACTTAA 202
QY 1884 GATGGCCCTGTATGACACAGGAATAACCAACAGGTTTATCTGAAGACCCAGGTAAGAT 1943
DB 201 GATGGCCCTGTATGACACAGGAATAACCAACAGGTTTATCTGAAGACCCAGGTAAGAT 142
QY 1944 GTTAATCTCCAGCCCACTCAACCCAGAGGCTACTCTTGACTTAGACCTATACTGAAAG 2003
DB 141 GTTAATCTCCAGCCCACTCAACCCAGAGGCTACTCTTGACTTAGACCTATACTGAAAG 82
QY 2004 ATCTCTGTGCATCCAACTGGAAATTCAGGAACCAAAAGAGCA 2048
DB 81 ATCTCTGTGCATCCAACTGGAAATTCAGGAACCAAAAGAGCA 37

RESULT 14

US-10-017-754-4/c

; Sequence 4, Application US/10017754

; Publication No. US20030054363A1

GENERAL INFORMATION:
APPLICANT: Henderson, Robert A.
APPLICANT: Wang, Tongtong
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Johnson, Jeffrey C.
APPLICANT: Retter, Marc W.
APPLICANT: Marnerakis, Margarita
APPLICANT: Carter, Darrick
APPLICANT: Fanger, Gary R.
APPLICANT: Vedwick, Thomas S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: McNabb, Andria
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.478C18
CURRENT APPLICATION NUMBER: US/10/017,754
CURRENT FILING DATE: 2001-10-29
NUMBER OF SEQ ID NOS: 2004
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 510
TYPE: DNA
ORGANISM: Homo sapiens
US-10-017-754-4

Query Match 10.8%; Score 405; DB 9; Length 510;
Best Local Similarity 100.0%; Pred. No. 1.8e-195;
Matches 405; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 TGTGGAATATAATAGCTGAACTAACTACTGTACATAAATCCAGAGGACTCTGCTT 1703
DB 441 TGTGGAATATAATAGCTGAACTAACTACTGTACATAAATCCAGAGGACTCTGCTT 382
QY 1704 AAACAAGCAGTATATAAATCTTATTCATATAGATTAGTTTGTAACTTACTTTA 1763
DB 381 AAACAAGCAGTATATAAATCTTATTCATATAGATTAGTTTGTAACTTACTTTA 322
QY 1764 TTTTCTTTCTGGAATGGAATAAATCTCTCAGTATCCAGATTAATGCTCC 1823
DB 321 TTTTCTTTCTGGAATGGAATAAATCTCTCAGTATCCAGATTAATGCTCC 262
QY 1824 TTGTGCTCTTTTATTAAGTGGGTAGAGTAGTTTATTAATCAATCAAACTTAA 1883
DB 261 TTGTGCTCTTTTATTAAGTGGGTAGAGTAGTTTATTAATCAATCAAACTTAA 202
QY 1884 GATGGGCTGTATGACAGAGGAAACCAACAGGTTTATCTGAAGACCCAGGTAAGAT 1943
DB 201 GATGGGCTGTATGACAGAGGAAACCAACAGGTTTATCTGAAGACCCAGGTAAGAT 142
QY 1944 GTTAATCTCCAGCCCACTCAACCCAGAGGCTACTTTGACTTAGACCTATCTGAAAG 2003
DB 141 GTTAATCTCCAGCCCACTCAACCCAGAGGCTACTTTGACTTAGACCTATCTGAAAG 82
QY 2004 ATCTCTGTCACATCAACTGGAATTCAGGAAACCAAAAGCA 2048
DB 81 ATCTCTGTCACATCAACTGGAATTCAGGAAACCAAAAGCA 37

RESULT 15
US-09-864-761-21309/c
Sequence 21309, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Aemica-x-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312

PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
SEQ ID NO 21309
LENGTH: 219
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC012119.1
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.7
OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 2.4
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.8
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.8
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.4
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.1
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.8
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.7
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.2
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.7
OTHER INFORMATION: SWISSPROT HIT: P52823, EVALUATE 2.00e-36
OTHER INFORMATION: NT HIT: AF098463.1, EVALUATE 1.00e-120
OTHER INFORMATION: EST_HUMAN HIT: AW954342.1, EVALUATE 1.00e-116
US-09-864-761-21309

Query Match 5.6%; Score 212; DB 10; Length 219;
Best Local Similarity 100.0%; Pred. No. 3.3e-97;
Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 435 GGAAGGATTCGTCAGAGAGAGCTTAAATGTCATCGCAACGGGGTCACTCCCAAGGTC 494
DB 219 GGAAGGATTCGTCAGAGAGAGCTTAAATGTCATCGCAACGGGGTCACTCCCAAGGTC 160
QY 495 TTCCTCGCCATTCGAGAGGTGCTCCACTTTTCCAAAGGATGATTGCTGAGGTGCGAGGAAG 554
DB 159 TTCCTCGCCATTCGAGAGGTGCTCCACTTTTCCAAAGGATGATTGCTGAGGTGCGAGGAAG 100
QY 555 TGCTACAGCAAGCTGAATGTGTGAGCATCGCAAGCGGAACCCCTGAAGCCATCTACTGAG 614
DB 99 TGCTACAGCAAGCTGAATGTGTGAGCATCGCAAGCGGAACCCCTGAAGCCATCTACTGAG 40

Qy 615 GTCGTCAGTGCCTCAATCACTTCTCCACAG 646
|||
Db 39 GTCGTCAGTGCCTCAATCACTTCTCCACAG 8

Search completed: June 12, 2003, 19:53:54
Job time : 500 secs